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RIYYKOMESMI.KSEJERISI ÖNEYSKLILINI EHMSI.KALEVVMATYSKSI SÖNILIS
GTDI,SEFWI ILIVLNI.KALDIFYKVI ESE I KARĞULTEKIM KALLEKÇEHK IMESILAMLSI
SEJLFDLIKQSKDKEĞPTDHLESACPLNI.PIQNNHTAADMYLSPVRSPKKKĞSTTRVNS
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/codou_start=1
/product-"retinoblastoma suspectibility protein"
/protein_id-"AAH59465.1"
/db_xre1-"G1:793995"
/db_xre1-"GDB:G00-118-734"
                                     /note-"Timor GOS537 bilateral trameshift mutation causing premature stop.; GOO-118-734" /citation [5] /replace "c"
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/replace="ca"
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/replace="ta"
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/note-"Tumor GOS561 unilateral trameshift mutation causing
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537, .542
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RVLKKSAFGSNTPKPLKKILKEDTEGSDEADGSKHILPGESKFOOKLAEMTSTRTRMQKQ
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999. .1076
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1353. .]469
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1577	GAGAAGAAGAACATTATCCATTCAAAATTTTTAGCAAACTTCTGAATGACAA		90
403	erGluGluGluArgLeuSerfleGlnAsnPheSerLysLeuLeuAsnAspAs		γο
1517	ANTIGGACTACAAGGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCAT	_	B 3
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363	HyTyrtlePhetysChiLycPheAlaLysAlaValGlyClnGlyCysValo		Q.
343 1397	YrPheAsnAsnCysThtValasnProtysGluSorTlet.cutysArgVall 		4c 4c 4c
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303 1277	AA — As		4d 45
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163 857	"UASPTYLPHELLELYSLEUSEEPFOPFOMETLEULEULYSGLUPFOTYFLY - - - - - - - - - - - - - - - - - - -	798	4c 4c
143 797	ysdlydluValleudluMetGluAspAspleuVallleSerPheGluLeuMetLe 	738	4d 40
123 737	eSerThrölmileAsmSerAlaLemValLemLysValSerTrpileThrPheLemLe 	678	£ &
103 677	LeupheSerfysteuGluArqfbrCysgluteuflefyrteufhrGfbpr 	818 818	40 40
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Qy 44 nLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThrSe	Oy 32	Db 243 TICATCIGIGIATGRAGTATIGRAGARITATATICAAAAGAAAAAGGAACTCIGIGAAT	оу 41	QY 31	Db 123 CCTGCCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTTACTGCATTATG	Oy 21 ProAlabro-ProProProProProProProCluVal IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY 1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaAlaGluPro 1 (1 (1 1 1 1 1 1 1 1 1	97.75% Indels: 6 Gaps: 851) x 109369 (1-4597)	Prod. No. 1.12c-31C Length: 4597 Score: 4283.50 Matches: 848 Percent Similarity: 91.38% Conservative: 0 Best Local Similarity: 91.38% Mismatches: 3	BASE COUNT 1489 a 841 c 813 g 1454 i ORIGIN	õ	Unclassified. 1 (bases I to 4597) 1 (bases I to 4597) Dryja.T.E. Friend.S. and Yand DIAGNOSIS OF RETINOBLASTOMA	VERSION 109369,1 GI:587899 KEYWORDS : KEYWORDS : VIJECE	109369 109369 No. 1	14 11 11 11 11 11 11 11 11 11 11 11 11 1	2838 843	2778	971B	Db 2658 GACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAACGAAAAAAAA
64 Qy	09 10b 1	302	31 Qy	31 Db 1	31 Db 1	31 Oy Db 1	20 Qy Db 1	. Oy 26	Cy 24 Db 96	27 2 Db 9	. DP 8	,	Qy 1	PAT 02-DEC-1994 DE	Ο _γ 1	2897 QY	2837 Oy	2777 Oy	2717 Db
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2103 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT
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2523 TECTHANAMITECOMIANATANATOMIATISTATGEACAGIGMIGITGCTCAAAAG 2582
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152 LeuSerProFroMetLeuLeuLysGluProTyrLysThrAldVall1leProlleAsnGly 171
                           824_uAlaGluMctThrScrThrArqThrArqMctGlubysGlubysMctAsnAspScrMctAs_B44
                                                     132 GluAspAspLadVullleSerPLeGlt.LadMethadCysVulladAspTyrPhelleTys [15]
                                                                                   247 TT66TGCTAAAA6TTTCTT6GA1CACATTIIIAITAGCIAAAGGGGAAGIAIIACAAAIG
                                                                                                                                       92 Cys@luLeuIleTyrLeuThrGlnProSerSerSerIleSerThrGluIleAsnSerAla 111
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                                                                                                                                                                                                                                                                                                                      7 GACCTAGATGAGATGTCGTTCAGTTTTAGTGAGCTAGAGAAAAACATAGAAATGAGTGTC 66
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AR072031
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331 906	312 LeuAsnSerAlaSerAspGlnProSerGluAsnLeuIleSerTyrPheA 	₽ .č
311 846	292 ILGETOFTOHISTHTPTOVALARGTHTVALMGTASmThtlied 	왕
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271 726	252 LysAspLenAspAlaArqLenPheLenAspHisAs 	941 A&
251 666	232 ASHC1YLCUPTOC19V31C19VASH1CUSCHLYSATGTYTGTUG1u11cTYT 	함
231 606	212 LysAsnValTyrPheLysAsnPhoIleProPhoMetAsnSerLoug) 	94 64
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  Chadim, Z.,
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                   4 (sites)
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                                                                                                                                         Oncogenic point mutations in exon 20 of the RMI gene in families
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  and Cowell, J.K
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Cowell,J.K. and Kaye,F.J.
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Molecular mechanisms of oncogenic mutations in tumors from patients
with bilateral and unlateral retinoblastoma
Proc. Natl. Acad. Sci. H. S. A. 90 (15), 7351-7355 (1993)
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Br. J. Cancer 68 (5), 958-964 (1993)
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                                                                                                                            /note-"Tunor GOS19 unilateral mutation causing a tentative wrong splice; G00-118-734" /citation=[5]
                                                                                                                                                                                                                                                                              RVLIKEEEYDSIIVEYNSVEMQRLKTNILQYASTRPPTLSPIPHIPRSPYKEPSSPLR
IPGGNIYISPLKSPYKISEGI.PTPTKMTPRSRILVSIGESFGTSEKEQKINQMVCNSD
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SPLFULIKQSAUKFGFIUHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHITWT
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LFLDHDKTLQTDSIDSFETQRTPRKSNLDEEVNVIPPHTPVRTVMNTLQQLMM1LNSA
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MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRTPRRGQNRSARIAKOLENDTRIIEV
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/protein_id="AAH59465.1"
/db_xref="G1:793995"
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621, .622
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/note-"G00-118-734"
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                                                                                                    premature stop;
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premature stop; G00-118-734"
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Oy 542 GITCGATA ICTAC IGAAATTAAATTCTGCATTGCTGCIAAAAGTTTCTTGGATCACATTTP 601 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII			Voumber-13 variation 14001401 Query Match 94.4%: Score 3194.6; DB 9; Length 4839; Best Local Similarity 95.1%; Pred. No. 0; Matches 478; Conservative 0; Mismatches 4; Indels 171; Gaps 1; Matches 478; Conservative 0; Mismatches 4; Indels 171; Gaps 1; 09 2 GOUTGATGPCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	/denemb1 /notemb1//most GoSi3 unilateral trameshift mutation resulting in premature stop: Associated with this mutation is a large [3q14.3 sub-band deletion; G00-118-734" /reflation=[5] /replace-"ca" 1853. 1469 /denemg00 [18 734"	variation 1420 /number=12 /number=12 /note-"RBI" /dene-"RBI" /note-"Tumor (AuS559 mutation causing premature stop.: 600-118-744 / /ceitation=54 / /ceptace-"("
Oy 1451 AAGGCAACTIGACAAGAGAATAAAACATTIAGAACAATIGATAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATATIGAACAATAACAATAAACAATTAATTAATTAATTAATAAACAATAAACAATAAT	1271 1573 1331 1633 1391 1693	Db 1273 TGAACACTA CCACCACTTAATGATGATTTATATTTATATTTATATTTATATTTATATTAT	Db 1093 AACGAHACGAAGAAAFFFTATCTTAAAAAAIAAAGAFCTAAGAGAFTATITITICGAAGAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 973 ANGANCALGANIGIANIAGANGHGANAAATGITIATITCANAANTTTTAIACCTT Oy 731 GGTGGAATTCTCTTTGGACTTGTAACACCTAATGGACTTCCAGAGGTTGAAAACCTTCTA LILITHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Db 853 ATAAAACAGCIGTIATACCCAITAAIGGIICACCICGAACACCCAGGACACCCAGACACCCAGAACACCAGGACACCCAGAACACCAGGACACCCAGAACACCAGGACACCCAGGACACCCAGAACAAGAAG

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    Friend, S.H., Horowitz, J.M., Gerber, M.R., Wang, X.F., Boronmand, i.
Li, F.P. and Weinberg, R.A.

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/db_xref="taxon:9606"
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Dryja,F.P. and Friend,S.
Humus DNA in the diagnosis of retinoblastoma
Patent: EP 0259031 A2 1 09-MAR-1988;
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BASE CONTIGIN ORIGIN OBERTHESE HEST MATE	BASE COUNT 1489 a 842 c 812 q 1454 t ORIGIN ORIGIN 93.6%; Score 3165; DB 6; Length 4597; Hest local Similarity 95.0%; Pred. No. 0; Matches 3372; Conservative 0; Mismatches 5; Indels 174; Gaps Oy 4 GTCATGCCGCCCAAAAACCCCCCGCGCGCGCGCGCGCGCG		04 A0 40 40 40 40 40 40 40 40 40 40 40 40 40	958 CGATACGANGANATTATCTTANAALAAAGALCLAGALGCANGALLAFTTTTTGGATCAT 853 GATAAAACTCTTCACACTGATTCTATAGACACACTTTTGAAACACACAGAGAACACACCACAACAACACACAGAGAACACACAGAGAACAAC
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37	GANATTOGATO.CAGCGATACAACCTTGGACTTCGCTTGTATTACCGACTAATGGAATCC	<u></u>	D.
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25	VITITAACAACTGE ACAGTGAATCCAAAAGAAAGTATACTGAAAAAGAGTG	, 1148	5
1092	CTGATTTCCTATTTTAACAACTGCAAAAGTACAACTGCAAAAGAAAG	. 1033	γ.
1197	ANY AY TATECAAY AATLAATGATGATTTAAATTCAGCAAGGATGATCAACCTTCAGAAAAAT ANY AY TATECAAY AATTAATGATGATTTAAATTCAGCAAGGATGATCAACCTTCAGAAAAAT	11148	탈
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957	TO MATTE TESTINATES TANTED AND TESTINATES AND TESTINANA	898	F &
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732	00	7 3	Ç.
837	TGCACGGATAGCAAAACAACTAGAAAATGATAGAAGAATTATTGAAGTTCTCTGTAAA		dq.
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777	- IGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAGG	718	Εb
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	HITATIAAACTCTCACCTCCATGTTGCTCAAAGAACCATAT		말.
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	GCACTCTTCAGCAAATIGGAAAGGACATGTGAACTTATATATATTTGACACAAGCCAGCAGT 5	. 4	γυ
7	ACCAGIACCAAAGITGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTT 4	418	Ę
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                                                           CAGAATGTAAAAGAACTTACTGATTATTTTCTTCATCCAACTTATGTTTTTAAATGAGGA
                                                                                                                                                                  AGCTGGAAGCAAAGTATAACCATAEGATACTATCATACTGAAACAGATITCAIACCT 3312
FIAFFGATAGT 3548
                                TIATIGATAGE 3383
                                                                                                                                 AGCTGGAACCAAAGCATATGATACTATCATACTACTACTGAAAACAGATFTCATACCT
                                                                                                                                                                                                                                                                                                                                                                                                                          GICTGACTACTTTGCCTTCTTTTGTAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAA 3177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGICTAAAICCTCCCATTTAAAAAGTIGTAGCAGATTGTTTCCTCTTCCAAAGTAAAAT 3057
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Matches 3370;

Best Local Similarity 94.8%;

Conservative

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                                         1038 bp upstream of EcoRI site; chromosome 13q14.1.-{14.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Draft entry and computer-readable copy of sequence in (1) kindly provided by R Heekstein, 27-APR-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pukaryota; Metuzoa; Chordata; Craniata; Vertebrata; Enteleast mi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 24) to 4740)

Lee.W.H., Bookstein,R., Hong,E., Young,L.J., Shew,J.Y. and Lee,E.Y. Human retimeblasiona susceptibility gene. cloud,A. identification.
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Homo sapiess (close: RB [125]) Loctus tetina (SNA to mENA
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FVLIKFEEYDSTIVFYNGVEMQELKTNILQYAGTREETLSIIFHIEKSEINFESSELK
IPGGNIYISPLKSPYKISEGLETPTKMIPRGRHIVSTGESGVHSEKEÇKINQMVASO
                                                                                              KMNDSMDTSNKEEK"
                                                                                                               RVLKRSAFGSNPPKPLKKLRFD1EGSDEADGSKHLPGESKF@@KLAEMTS
                                                                                                                                                                                                 SPLFBLIKOSKDREOPTBHLESACPLILFLOUNHIAALMYLSEVESEKEEDSTIERUS
TANAETOATSAFOTOKEIKSTSESLEYKEVYKLAYLKUNILCEKLISEHTELEHTIMI
                                                                                                                                                                                                                                                 GPDLSFPWILINVI.NI.KAFDFYKVIESFIKAEGNLFREMIKHLERCEHRIMESLAWLSD
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MICVLDYFIKI.SPPMLLKEPYKTAV1P1NGSPRTPRRQQNRSAR1AKQLENDI K11FV
LCKFHFCNIDEVKNVVEKNFIDEWNSLOTVISWOLPIVENLSEEYEE1VLKAKJIJHK
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                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MPPKTPRKTAATAAAAAAEPPAPPPPPPPPEEDPEUDSGHEDLEL
VRLEPEETBEPDETALCQKLKIPDHVREPAWLIWEKVSSVIAVIGAYJUKKELMGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA69807.1"
/db_xref="G1:190959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"retinoblastoma susceptibility protein"
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139. .2925
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/dov_stage="fectus"
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/db_xref="taxon-9606"
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1152	AAACGATACGAAGAATTTATCTTAAAAATAAAGATCTAGATCGAAGATATATTTTTGGAT	104	Þ
849	AAACGATACGAAGAAATTTATCTTAAAAATAAAGATGTAGATGCAAGATTATTTTTGGAT	74(Ϋ́O
1092	TTTA FGAAT TETETGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAATCTTTCT	103	41
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1033	ANAGAACA IGAA IGTAA IA IAGA IGAGG IGAAAAA IGT FEA LI IGAAAAA ETI ETATAGGT	4.7	Ē :
740	The state of the s	7 :	5 .
470	AGGAGUGTAGGAAAAGTAAAGTAAGAAAAAAGTAAGTAAG	<u> </u>	<u>.</u> 5
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730	TATAAAA'AA:	721	Yo.
852	A IGC FATGLIGGET GACTALLITATIAAACTCTCACCTCCCAGULIGGICAAAGAACCA	79.	126
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660 792	TTAT FAGE TAAAGGRAAGTA ITAGAAATGGAAGATGATCIGG IGATTTIGATTTIGAGTTA HILLIH	73	95 A
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361	GGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTG	302	Š
301 433	AGAAAGHERGA GUGUGGAAAGAAGAAAAAGGAAGCTGT {	242 374	£ 5
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1930 CATTTGAYC'AAATTATGATGTTCCATGTATG3CATAT& AAAATAAAAATATATATGATGTTCCATGTATG3CATATATATGAAATTATATATATGTTCCATGTATGTATGT	δ. δ.	
1870 ATCATCTS -A-YSCITITECAAS/A-YGS OS WAAADGASTALAAN TEALSANAASANAA AASA HIIIHHII ATHIIHHIIHHIIHHIIHHIISI HIIHHIISI HIIHHII ATAA OS WAAAGANAA WAA AASANAA AASANAA OS ASANAANAA AASANAANAA AASANAANAA AASANAANAANAA AASANAANAANAANAANAANAANAANAANAANAANAANAA	4d 40	
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1750 CAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTAAAAAAAA	dd VD	
1690 ACTACGCGTGTAAATCCTACTGCAAATGCAGAGACACAAGCAACCTCAGCCTCAGCCTCAGACCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCACAAATGCAGAGAGAAAAAAAA	4d 4b	
1630 AATCACACTOCASCAGATATGTATCTTCTCCTGTAAGACCTCCGAAACAAAAACCTCT HITHHITCT HITHHITHHITHHITHHITHTHTTTCTCCTGTAACATCTCCCAAACAAAAAAAACCTCTCTGAAAAAAAA	Oy Db	
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1510 GAATCCCITGCAIGCCTCZAGATTCACCHIAHIIGAICTIAHAAACAAF AAAGSAC HIIHHIIHHIIHHIIHHIIHHIIHHIIHHIIHHIIHHI	106	
1450 GAAGGCAACTIDACAAGAGAAATRATAAAAAPATTTADAACGABEDGAACABCCAAB 	Db Db	
1390 AATGTGCITAAITTAAAAGCCITTGAITITTACAAAGGATGAIGAAGTTTTATCAAAGCA 	4d	
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1270 GACAACATTITICATATGUCTITATIGGCCTGGCCCCTIGAGCTGGAAGAGAGACATATATATATATGGCCTGGCC	da Ao	
12.10 TCCATGCITAAATCAGAAGAAGAACGATIATCCATTCAAAA1111AGCAAACHTCTGAA HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Qy Db	
1150 GTCGAAATTGGATCACAGGGATACAAAACTTGGAGTTGGCTTGTALTACCGAGTAAACGAAGAAA 	901 60	
1090 GIGAAGGATATAHAHAHAHAHAHAHAHAHAHAHAHAHAHAHA	ob	-
10.30 AATGTGATTTGCTATFTTAAGAACTGCACAGTGAATGCAAAGAAAGAAAGTATACTGAAAGA 	dd VQ	
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                                                                                                                                           2950 COLORICTORACTACTETIGCCTTCTTTIGTAGCALATAGGTGAGGTTTTGTGTTGTTTTTTAT 3009
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                 ATCITCCAAATGCAATTGATTGACTGCCCATTCACCAAAATTATCCTGAACTCTTCTGC 3129
                                                                                                        TAATTTATATGTATATTTTTTAATTTAACATGAACACCCTTAGAAAATGTGTCCTATCT 3069
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391 CATAAATICTIIAA0.01A0.01AAA0.00AAA0.00AA0.00A0.00A0.00AA0.00A0.00A0.00A0.00
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Local Similarity 94.5%;
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Xu,H.J., Hu,S.X. and Benedict,W.F.
Broad-spectrum tumor suppressor genes, gene products and methods
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227	del *	359	390 PSCOTETIGAGGIIGYAATGCCCACATALAGCAGAAGIACATCLCAGAAFCTTGATTCL L	S
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1267 T	Ov Db	570	511 IGIGAACI:AFAFATTIGACACAAGCAGCAGTTCGAFACTGAAFAAATTCTGCA - - - - - - - - - - - - - - - - - - -	qq Ağ
1207 (0v D	186	451 FUNAGACTGTTGANGANGTATGATGTATTGTATTGCACTCTTCAGCAAATTGGAAAGGACA 	B 8
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TITLE
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Best Local Similarity
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                                                                                     2510 CACACTILLICAAACACAGAGAAAACACCAGGAAAAAGTAACCTTCATGAAGAGACTTTAATGTA 245
                                                                                                                                                                              2690 AAAAATGTTTATTTCAAAAATTTTATACCTTITATGAATTCTCTTGGACTTGTAACATCT 263
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                                      940 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTATCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                      Xu,H.-J., Hu,S.-X. and Henedict,W.E. Broad Spectrum tumor suppressor denes for tumor suppressor gene therapy Fatent: US 5496741-A 2 05-MAK 1996;
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2079 1311	AAGGAFCTICCTGCAGGTGTFCAGGAGACATTCAAACGTGTLTTGATCAAAGAAGAAGAGGAG	8
2019 1371	TATESCATATECAAACTGAACAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACTCLICICICLICICICATACTGTAACACCATACATATGTAACAGCATACATATGTAACAGCATACATA	章 8
1959 1431	1900 CANAATRABRATRAACTCATRAGAGACAGGCATTIGGACCAAATTATGATGTGTTCCATG 	£ 5
1899 1491	CTTOTATOTAGAGCACCAC	ψy
1839 1551	CTGTTTTATAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACA	D).
1779 1611	GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCAT [<u> </u>
1719 1671	요필요	\$ 44 An
1659 1731	GUTTGTCCTCTTAATCTTCCTCTCAGAATAATCACACTGCAGCAGA	B 68
1599 1791	TTATTERATCTTATTAAACAATCAAAAGGACCGAGAAGGACCAACTGATCACCTTGAATCT	\$ ×
1539 1851	CALILAGAACGA IGUGAACA ICGAA ICATGGAATCCCTIGCA IGGCYCYCAGATYCACCY 	₽ \$\disp\disp\disp\disp\disp\disp\disp\disp
1479 1911	TACANAGTGATCGAAAGTTITATCANAGCAGAAAGGCAACTTGACAAGAGAAATGATANAA	98 88
1419 1971	1360 SGAACAGATITGICITTCCCATGGATICIGAATGIGCITAATITAAAAGCCITTGATFIT 	90 VQ
1359° 2031		qq VV
1299 2091	CCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCG 	46
1239 2151	SÖAGI FOGULIGIALI ACOGAGI AALGGAA FOCATGOTTAAATCAGAAGAAGAAGAACGATTA FEH HELLIH HELIH HELLIH H	<u> </u>
1179 2211	TOWNOVALWEGGENCOSTRESSTENCES	F S
1119 2271	J. I. GAAA I C. AAAAA RAAR HALAY HAAAAARA ELRAARRA LALARRA LALACA I CLI LIAARAAR HALAKHI HALIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	F 8
1059 2331	ITAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA	S &

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482 TTGCACTCTCAGCAAATTGGAAAGGAAAGGACTTATATATA	OY 422 ALACCADACCADACCADA CAAAAAGI IGA IAATGO ALGI CAAGAGACIGI IGAAGAAGIA IGAIGAIGTAITGI 481 HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	UY 462 AGCTACAGAAAAACATAGAAATCAGTGTGCATAAATTGTTTAACTTACAAAAAAAA	OY 402 GGGGAATCTGTATCTTTAITGGAGCAGTIGACCIAGATGAGGTCACTTCACT		CATTALLELE HADAGAAATTAAAGALAACGADA DA GEGAGAGAGAGAGAGAGAGAGAGAGGEGGGGGGGGGG	QY 122 CGGARGACCTGGCGCGCGCAGGCTTGAGTTTGAGAGAAACAGAAGAACCTGATTTTACTG 181 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	62 AACCECCUSEANCGECCUCICACIGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	CCGAAAAACGGCCGCCACTGCCGCGCGCTGCCGCGCGCGC	Obery Match 74.0%; Score 2502.6; DB 6; Length 2994; Best Local Similarity (9.7%, Bred. No. 0; Matches 2686; Conservative (0; Mismatches 4; Indels 171; Gaps 1;	N .	Antelman, Retinoble Ratent: 1	ž	KEYWORDS ANDYRIBY: GITTEROXAGE SOURCE Unknown.	ION Sequence 3 from patent US 6074850.		QY 3440 TITETTEATECAACTIATGITTITAAATGAGGATATTGATAGI 3383 HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	US 4280 TACTATCATACTGAAACAGATTTCATACCTCAGAATGTAAAAGACTTACTGATTAT 4339 	OY 3220 TOTTTATAAAAFTTTOOTIFTAATFAAATAAAAGCTGGAAGCAAAGTATAACCAFATGA 3279 	
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{f 5}^{f 6}{f 4} ATACOAGTACOAAACTTOATAATCOTATCOAACAACCOTOTTOAACAAGTATGATGTATIGI{f 6}{f 1}
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Sequence 3 from patent US 6379927
AR207831
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Antelman,D., Gregory,R.J. and Wills,K.N
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1450 1753	ATGTGCTTAAITTAAAAGCCTTTGAITTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAG 	1 891	<u> </u>
1390 1693	GCAGAAGTACA ECTOAGAAGCTTGA FECEGGAACAGATTEGGCTETTCCCATGGATTCTGA LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL		ê ş
1633	ACAACAT II FECATA IGEOTTI ATTGGGGGGGGGGTGT GAGGTTGTAATGGCCACATATA LLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	1271 1574	ê Å
1270 1574	CCATGCTTAAATCASAASAASAAWSATTATCCATTCAAAATTTTAGCAAACTTCTGAATG	1211	휴 · 호
1210 1513	TOGAAAT HIGATOAYAGOGATACAAACHTIGGAGTEGGCTTGTAFTACCGAGTAATGGAAT 	1454	ОУ
1150 1453	FGAAGGA LA FAGGA FACA FE ET LAAAGAGAAA E FIGET AAAGCTGTGGGACAGGGTTGTG	1091	44
1090 1393	ATCTGATTTGCTATTTTAN'ANCTGCACAGTGAATCCAAAAGAANGTATACTGAAAAGAG 	1031	9d 6A
1030	TGAACACTATICCAACAATTAATGATGATGATTTAAATTCAGCAAGTGATCAACCTTCAGAAA 	971 1274	94 85
970 1273	AAAGWAACCTTGATGAAGAGGGAAAGGAATGTAATTCCTCCACACACA	911 1214	Οy
910 1213	ATGATAAAACECTTCAGACTGATTCTATAGACAGTTTTGAAACAAAAAAAA	851 1154	gg A
850 1153	AANATANWAAGAAFT FATOTTAAAAATAAAGATCTAGATGCAAGATTAFTTTTGGATC 	791	Qcl VQ
790 1093	GAALTICTICTICGACETIGTAACATCTIATATGGACTTCCAGAGGTTGAAAATCTFTCTA TTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAATCTTTCTA	7 45	рь
1033	AAGAACA HGAA HGTAATA FAGA HGAGG HGAAAAAA HGT FLATT FCAAAAACT FTAHACCTT	974	9
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7 4 4 9 7 3	UGACTES ANGGA LAGYAAAACAACTAGAAAATGATACAAGAA ITATTGAAGTICTICTIGTA	735	90
913	ATANAN 'NE TGTTATAGCCATTAATGGTTCAGCTCGAACACCCAGGGGGGGG	#54	₽ 5
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661 793	FAT FAGY FAAAGGGGAAGTA EFACAAA FGGAAGA GA FCTGG FGATT FCATTTCAGTTAA 	502 744	94d
601 733	GTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTT	542 674	dd An

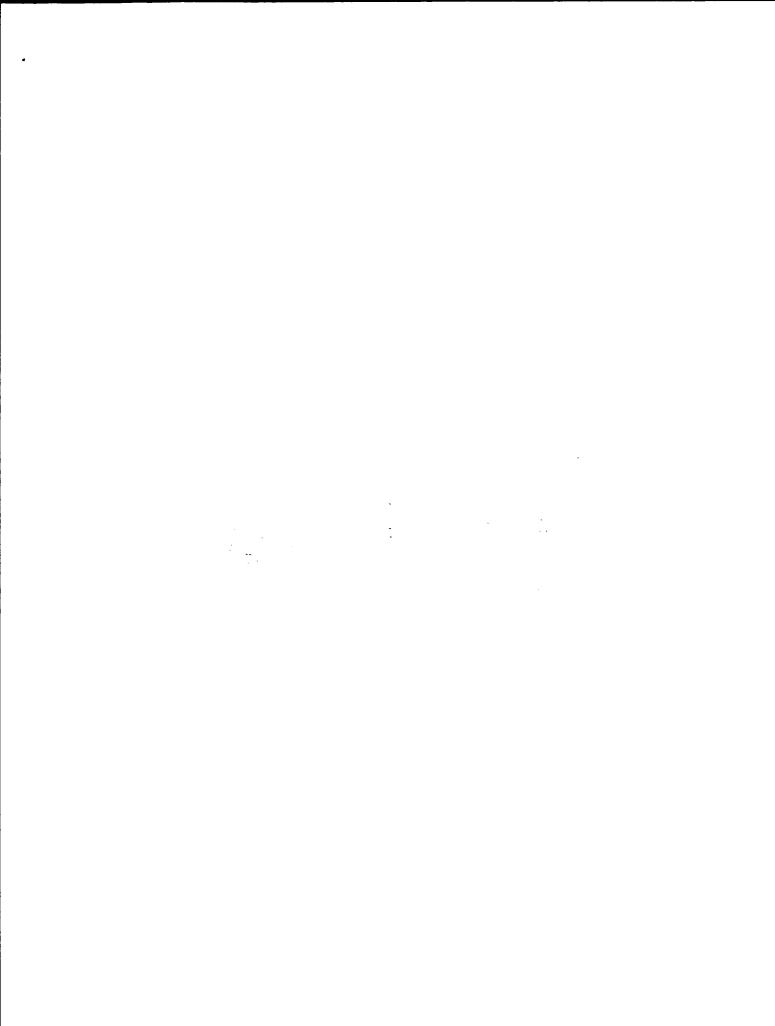
1631 1934 1994 1751 1994 1811 1811 1931 1931 1931 2294 2051 2354 2414 2534 2534 2534 2534 2534 2534 2534 253	Db 2774 TTGAAGGATGAGAAGAAGAAGAGAGAAGAAGAAGAAGAAAAGAAAATTA AG Uy 2531 AGAAACTGGAAGAAATGACTTCTACTGGAAGAAGGAATGGAAAAGAAAAAAAA
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                                                               374 AGAMMUTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAMMGAMAMAGGAMCTGT
                                                                                                                            122 GGGAGGACCTGCCTCTCGTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTG 181
                                                                                                                                                                                                                                                                                                                     AGAAAGITTCATCTGTGGATGGACTATTGGGAGGITATATTCAAAAGAAAAAGGAACTGT 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS COTHELY 94 COTKS ZOO, NGLE (B, YOU, AGLE Y, TE CO CO Strandedness: Single; CC Topology: Linear; Location/Qualifiers FH Key Location/Qualifiers FI source /organism-'Unidentified'.
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Fissue specific expression of retinoblastoma protein 
Patent: JP 2001503638-A 2 21 MAP 2001;
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2410	35 L. PODRITACH POPORADAGO POCAGARAAA PAAA POAGA POTTA FOTAACAGAGAGAGGEGTGO	٨.
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1930 2234	371 TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGGGC 	K ==
1870 2173	### ATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTGTGAGCACCAGAATTAGAACATA 	K: =
1810 2113	751 AGAAGCATTGAAATCTACCTCTCTTCACTGTTTATAAAAAAGTGTATCGGCTAGCCT 	K: 1
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1690 1993	ER A FONCACH GEAGCAGATA I GLIA FOLL FOLCT GLIAAGA FOLCCAAAGAAAAA AGGIT GAA 	
1630 1933	71 GAGAAGACCAACTGATCACCITGAATCIGCITGTCCTCTAATCITCCTCTCCAGAATA 	.
1570 1873	SII AMPOOTTGCATGROTECRGATECAGATECACCTTATTTGATCTTATTAAACAATCAAAGAACC HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
1813 1813	151 AAGGCAACTIGACAAGAGAAAA GAIAAAAACATTIAGAACGATGIGAACATGGAATGATGG 	tab 1
1450 1753	991 ATGTGETFAATTFAAAAGECTTFGATTFITACAAAGTGATEGAAAGTTITATCAAAGCAG HEHLIJIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
1390 1693	## GEAGAAGIACA CICAGAATETIGATICTBGAACAGATITGICTTTCCCATGGATTCTGA 	
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                                                                        434 GGGGAATCTGTATCTTTATTGCAGCAGLIGACCIAGATGAGAIGIGGTTCACTTTTACTG 453
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                                                                                                                   242^{\circ} AGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGGAAACTGT^{\circ} ^{\circ} ^{\circ}
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SUMMARIES

ALIGNMENTS

11111K	AUTHORS	REFERENCE	OR COM LOS		KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	HUMRHA] RA	RESULT 1
Li,F.P. and Weinberg,R.A. Deletions of a DNA sequence in retindulastomas and mescachymal	Friend, S.H., Horowitz, J.M., Gerber, M.R., Wang, X.F., Bogenmann, E.,	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 4600)	nomo saprens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;	Homo sapions (clone: p4.7k) cDNA to mkNA.	retinoblastoma protein.	M33647.1 GI:190945	M33647 J02994	Human retinoblastoma associated (RBI) mRNA, complete eds.	HUMRBALRA 4600 bp mrna linear PFI 12 JUL 1995		

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TITTATTAAACTCTCACCTCCCATGITGCTCAAAGAACCATATAAAAACAGCTGTTATACC 737
                                                                                    ATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATGTGTCCTTGACTA
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VRLEFETEEPDFTALFQKLKTPDHVRERAWLTWEKVSSVTGVLGGYIGKKKELWGIF
IFIAAVDLDEMSFTETELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                     Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,C.
Horrigan,S., Soppet,D.R. and Weaver,Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinoblastoma patients using single strand conformation polymorphism analysis and polymerase chain reaction sequencing Oncogene 7 (7), 1445:1451 (1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  susceptibility deno
Gene 80 (1), 119-128 (1989)
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555 Univ. Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with bilateral and unilateral retinoblastoma Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7451-7455 (1994)
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Hr. J. Career 68 (5), 458-964 (1993)
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                                                                                                                                                                                                                                                      Ph: 416 813-5868
FAX: 416 813-4989
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/note-"G00-118-734"
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RVLKPSABGSNPPKPLKKLPFOIEGSDEADGSKHLPGESKFQQKLAEMISTRTEMQKQ
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LEQHT LQNEYELMRURHI.DQI.MMCSMYGI.CKYANI LILNEKI I VTAYKULEHAVQETEK
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/product-"retinoblastoma suspectibility protein"
/protein_Id-"AAB59465.1"
/db_xref="G1:793995"
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/note-"G00-118-734"
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1400. .140
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/citation-[18-734"
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÷ 4	1290 1652	PURGAANAGATERGINTERNOVARGAFINIGAARGIGNITAARETAAAAGO : 	349
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Pry)a,T.P. and Friend.S.
Human DNA in the diagnosis of retinoblastoma
Price: EP 0259031-A2 1 09-MAE:1988;
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3315 ATTAGAAAAA	Db Cu	OY 2010 AGAAGAGGAGTAFGATTCTATTATAGTATTCTATAACTGGGGTCTTCATGCAGAGAGAG	ob Vy
3255 TIGACTOCCC	Db Cy	OY 1950 AACAGCAFACAAGGAFCETCCTCAEGCEGEEGAGAGAGAGAGAGAGACATTCAAACGTGTTFTGAFCAA 2009 	del VV
3195 TTAATTTAAC	Db Cv	OY 1890 GTGTTGCATGTATGGCATATGCAAAGTGAAAGAATATAGACGTTAAATTCAAAATGATTGT 1949 	Db Cy
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UY 630 AGARCTAGANATGATACAAGAATTATTGAAGTICTCTGTAAAGAACATGAATGAATAT 629 UY 630 AGARCTAGANAATGATACAAGAATTATTGAAGTICTCTGTAAAGAACATGAATGTAATAT 854 UY 630 AGARGAGGTGAAAAATGTTTATTCAAAAATTTTATACCTTTTATGAATTCTCTTGAACTTCTCTTGAACTTTTATGAATTCTCTTGAACTTTTATGAATTCTCTTTGAACTTTTATACCTTTTATGAATTCTCTTTGAACTTTTATACCTTTTATACAATTCTCTTTGAACTTTTATACCTTTTATACAATTCTCTTTGAACTTTTATACCTTTTATACAATTCTCTTTGAACTTTTATACCTTTTATACAATTCTCTTTGAACAATTTTA 749 UY 690 TGTAACACTTAAAAATGTTTATTCAAAAATCTTTCTAAACGAATACGAAACGAAATTTA 749 LILLIALIALIALIALIALIALIALIALIALIALIALIAL	CS ON OTHER AND INCAMENTAL INTERPRETATION IN AND INCIDENCE SACIA 449 25 615 ATTACANATGGANGATGAT INSTITUTION ITENSIFICATION IN INCIDENCE 450 THI ATTACANATGGANGATGAT INSTITUTION ITENSIFICATION AND ACCOUNTY AND ACCOUNTY IN INCIDENCE AND ACCOUNTY IN INCIDENCE AND ACCOUNTY IN INCIDENCE AND ACCOUNTY AND ACC		Purery Match 97.0%. State 3224.4; DE 6: Length 4597; Best Local Similarity 99 RR; Fred No. 0; Matches 3228; Conservative 0; Mismatches 6; Indels 0; Ga Matches 3228; Conservative 0; Mismatches 6; Indels 0; Ga 10.1.1.1.11111111111111111111111111111	SOURCE Unknown ORGANISM Unknown Unclassified. HEFERENCE 1 (bases 1 to 4597) AUTHORS Dryjs.i.P., Friend.S. and Yandoll.D.W. 111LE DIAGNOSIS OF RETINOBLASIONA JOURNAL Patent: WO 8906703-A 1 27-JHL-1989; FEATURES Source 1. 4597/Oualitiers Source /organism-"unknown" HASE COUNT 1489 a 841 c 813 g 1454 t	HESULI 5 [19369 19369 4597 bp DNA linear PAT 02-DEC-1994 DEFINITION Sequence 1 from Patent WO 8906703. ACCESSION 109369 VERSION 109369.1 CI-587899	OY 3270 PACHAATTA EPITCTTCATCAAC PAHCITT ETAAAHGACCASTATTATAAGT 3323 DE 3495 TACTGATTATITTCTTCATCCACCAACTATGTTTTTAAATGACCATTATTGATAGT 3548
1875 TGCADATGCAGAGCACAAGCAACCTCAGCCTCCAGACCCAGAAGCAATCAAA.AACACTCAGCCTTCCAGACCCAGAAGCAAACCAATCAAATCAACTCAGCCTTCCAGACCCAGAAGCAAAACACACTCAGCCTTCCAGACCCAGAAGCCAATCAAAATCTAC 18710 CTCCCTTTCACTGTTTTATAAAAAAGTGTATCGGGTTAGCCTATCTCGGGTTAAAAAAAA	Db 1695 AGATTCACCTTTATTTGATCTTATTTAAACAACAAAGAACAAGAACAAAAAAAA	Db 1515 TCTTGATTCTGGAACAGATTGTCTTTCCCATCCAAGAGGAAGGA	Oy 1110 AFACAACTTGGAGTLGGCTTGTATTACCGAGTAAIGGAAICGAIGC FIAAAICAAIA 184.	מ-ם מ-ם א-א	Oy 810 TGA FIGTATAGAGAGAGTITTIGAAAQAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAAAAGTAAFITTIA FIGTATAGAGAGA ASA TITTI	©2 750 TOTTAAAAALAAACATOTAGATGCAAGATTALLITTIGGATGATGATAAAAOTTOTTOTAGAC 80 4 Db 975 TOTTAAAAATAAAGATGTAGAGAGAAGAAGATGATAAAAAATTAAAAAA

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                                                                     214 GCTATGTCAAGACTGTTGAAGAAGTATGATGTATTGTTTGCACTCTTCAG AAATTGGAA 273
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                                                                                                                                                                                                                                                                                                            94 GAGGTCGACCTAGATGAGATGTCGTTCACTTLACTGAGCTACAGAAAACATATAGAAATC 153
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AR072031

    (bases 1 to 3232)
    Xu,H.-J., Hu,S.-X. and Benedict,W.F.
    Broad:spectrum tumor suppressor genes gene products and methods for

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ICAGAAGGTCTGGCAACAG 	POCTTACGGATTCCTGGAG 	SCCCCTACCTTGTCACCAA 	PATAACTOGGICTTCATGO 	ARBARACATTOAAACGTG - - - - - - - - - - - - - - - - - - -	AATATAGACCITAAA ITCA 	AGAGACAGGCATTTGGAGG - - - - - - - - - - - - - - - - - -	ETAGAACATATCATCTGGA 	2000TAGCCTATCTCCGGG 	ETECAGACECAGAAGCEAT 	MAGGITTCAACTACGCGTG 	CITOCAGAATAATCACACTG CITOCAGAATAATCACACTG	rcaaaggacggagaaggag 	SGAATCATGGAATCCCTTG 	ATCAAAGCAGAAGGCAACT 	POGATICHAANGEGETTA - - - - - - - - - - - - - - - - - - -	PYCACATATAGCAGAAGTA 	PITCTGAATGACAACATTI
DCAACAAAAATGACT 	SGGAACATCTATATT 	ATACCTCACATTCCT ATACCTCACATTCCT	TACAGACTGAAAAGA CAGAGACTGAAAACA	STTTTGATCAAAGAA STTTTGATCAAAGAA	AAAATCATTGTAACA 	CAAATTATGATGTGT 	ACCCTTTTCCAGCAC 	CTAAATACACTETGT CTAAATACACTETGT	TYGAAATCTACCTCT 	STAAATTOTAOFGCA 	GCAGCAGATATGTAT 	CCAACTGATCACCTT 	GCATGGCTCTCAGAT 	PTGACAAGAGAAATG	AATTTAAAAGCCTTT AATTTAAAAGCCTTT	ACATCTCAGAATCTT 	TTTCATATGTC FFTA

OY 649 GAAAAATGITTATITEAAAAATTITTATATATCITTATGAAFTCTCTTGGACTTGTAACATC 698 [HILLIHITH HILLIHIH HILLIH HILLIH HILLIHIH HILLIH HI	ON AUTOCETACATE TERESTEAN ACCASE TO AN ACCASE AND AC	UY 219 GTCANGACTGTGAAGAAGTAATGTTTGCACTAGCAAAGTTGAAATGCTAT 218 DB 3171 CCATANATTCTTTAACTTACTACTACTAAAAGAAATTGATACCACTACCAAAGTTGATAATGCTAT 3112 UY 219 GTCANGACTGTTGAAGAAGTATGATGATTGTTTGCACTCTTCAGCAAATTTGGAAAGGAC 278 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Othery Match 97.0%; Score 8224.4; D8 6; Length 8232; Hest Local Similarity 100.0%; Pred. No. 0; Matches 4224; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 99 (GACCTAGATGAGATGTCGTTCACTTTACTGAGCTACAGAAAACATAGAAATCAGTGT 158 1111111111111111111111111111111111	NOTE OUT OF	RESHILL B ARO72042/c LUCHS APO72042 DEFINITION Sequence 2 from patent US 5912246. ACCESSION ARO72042 VERSION ARO72042.1 G1:7222920 KEYWORKDS LEKENDER
Db. 1611 ACTGTTTATANANAGTGTATCAGCTATCTC GG ACACH LICE AND ACT ACT TO THE ACTOR AND ACT TO THE ACT T	1791 : 1599 : 1731 : 1659 / 1671 / 16	OY 1419 ACATTTAGAACGATGAGAACATGAACATGAACAGGAAGGA	1239 G 2091 G 1299 T 2031 T 2031 T	1119 · 2211 · 1179 · 1179 · 2151 · 2151 · ·	Oy 939 TTTAAATTCAGCAAGTGATCAGCAAAATCGGATTCCATTTTAACAACTGACTG	OY 819 AGACAGHTTIGAAACACAGAGAACAGCAGAAAAAGTAACCHDAAGAAAAAGTIAACAAAAACH 828 HJHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 TITTCTTCATCCAACTIATGITITTAAAIGAGGATIATTGATAGT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGITAGCAGAITTGTTTTCTTCTTTTCCAAAGTAAAATTTGCTGTTGTTTTTATTGGATAGTAAGAAT 472
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3413073
                                                              Molecular mechanism of retinoblastoma gene inactivation in retinoblastoma cell line Y79
Figg. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
                                                                                                                                                                                                          2 (bases 1 to 480)
Lee, E.Y., Bookstein
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                                                                                                                                                                                                                                                                                                                                                                                    and sequence
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Mammalia; Eutheria; Primates; Cafarrhini; Hominidae; Homo
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Home sapions (clene RR [1,5]) feetus retina eDNA to mRNA
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                                                                                                                                                                                                                                                                                    3823889
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                                                                                                                                                                                                          Bookstein, R., Young, L.J., Lin, C.J., Rosenfeld, M.G
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Bookstein,R., Hong,F.,
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Best Local Similarity 99.8%;
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819 TAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAACAGCTGTTATACCCATTAA
                             579 TATGTCAMPANTGITGAMPAAGIATGATGTATTGITGCMCTCITGIGATAATGGAAAG 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 TATOTCAAGACTGTTGAAGAAGTATGATGTATTCTTTGCACTCTTCAGCAAATTGGAAAG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 TUTTULATAAATTUTTTAAVITTAVITAAAAGAAATTUAATAVIVAUTAOQAAAGTTGAITAATGO 215
                                                                                                                                                                                                                                                                                699 THEOTHER THE TANAMETT TO THE GATE AND TOTAL TRACTOR AND GOOGGAGINITACIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 GTTGACCTAGATGAGATGTCGCTCAC-TTTACTGAGCTACAGAAAAACATACGAAATCAG 518
                                                                                                                                                                                                          396. AANGGAAGANGANGNGGMGAMMPAAMMMCAGMAAAGCMAMGMCCMTGACTALINTAL 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 GTCGACCTAGATGAGATGTCGTTCACTTTACTGAGCTACAGAAAAACATA-GAAATCAG 155
                                                                                                                                                                                                                                                                                                                                                   TGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTAGCTAAAGGGAAGTATTACA
                                                                                                                                    AATGGAAGATGATTGGTGATITCATTICAGITAATGCTATGTGTCTTGACTATTIAG ou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braft entry and computer-readable copy of sequence in [1] kindly provided by R.Bookstein, 27-APR-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1838 by upstream of Booki Sibe, chromosome 13414.1 414.2.
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887 c 86
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TANAETQATSAEQTQKELKSTSLSLEYKKVYRLAYLRLNTLCEELLSEHEELEHIIWI
LEGHTLQNEYELMEDEHLIGIMMESMYSTEKKVIRLOKEEFIIVTAVETLEHAVQETEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RITYRVMESMLKSEEERLS I QNESKILNDNI FHMSILIACALEVVMA FYSRS I SQNIJDS
GTDLGFFWILINVLNIJKAFDFYKV I ESF I NAEGNILTKEMI NHLERGEHRIMESLAWIJDI
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LCKEHBCNI JEVKNYZFKNET I PFMNSLJEVEN LISPBT FVETVMITT (SCLIMMITLIDR
LFILHIDKT LQTESI JOSFET GREEKK NALDEEYN I I IFPBT FVETVMITT (SCLIMMITLIDR
SDQFSENL I SYFNNCTVNFKES I LKKKKULIGY I FKEKFAKAGOGGCVF I GSGAN KIGV
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/db_xref="GI-190959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVLTKEEEYDSTIVFYNSVFMORLKTNILQYASTRPPTLSPTPHTPRSPYKEPSSPLK
TP3GNTYTSPLKSPYKTSE3T PTPTKMETESPTTSPTLSPTPHTPRSPYKEPSSPLK
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VRLEFEBTEEPDFTALQQKLKTPDHVKERAMIJWERVSSVDGVIGGYIGKKKEIWGTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RB-[1,5]"
/tissue_type="retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVLKPSAFGSNPPKPLKKLPFDTFGSTFADGSKHIFGFSKFLQKLAFMTSTVTFMLKC
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1535 1898	476 ACCITIALI IGAICHAITAAACAAICAAAGGACGAGAAAGGACCAACIGAICACC HITHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
1475 1838	416 779	65 1
1415 1778	456 TITITACAAASTGATGGAAAGTTITATGAAAGGAGAAGGAAAGGAACTTGAGAAAAGAGAAA 	
1355 1718	FICTRAAACAGA FITGICTFICCCA IGGATCIGAATGIGCITAATITAAAACCT 	
1295 1658	GROUTGE GET TETTRANGETTETRANGREE ACATATAGEAGAAG IACATETEAGA. 	
1235 1598	ATTATCCATTCAAAATTITAGCAAACTTCTGAATGACAACATTTTCATATGTCTTATT	
1175 1538	ACTEGGACTECGCETGTATEACCGAGTAATGGAATCCATGCTTAAATCAGAAG,	
1115 1478	AGAGAAATTIGGTAAAGCTGTGGGACAGGGTTGTGGGAAATTGGATCACAGCGATA 	0y 1
1055 1418	CM'AGTGAATGCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATGTTT 	
995 1358	GATTHAAAHCAGGAAGTGATCAACCTTGAGAAATCTGATTTGCTATTTTAACAACTG	
935 1298	-, -,	OY 1
875 1238	TAFAGACAGTTITTGAAACACAGAGAGACACCCGGAAAAAGTAACCTTGATGAAGAGGGGAA 	
815 1178	AAA FAAACA DETAGA DECAAGA FIA LEEL DEGATCA DEATAAAAC TETTEGAGACTIGATTE LEELEELEELEELEELEELEELEELEELEELEELEELE	
755 1118	A POTRA FOCACOTTOCACAGGOTTGAAAA FOTTTOTAAAGGA FACGAAGAAATTTATCTTAA 	
695 1058	6.46 GGTGAAAAATGETTATTECAAAAATTTTATACCTTTTATGAATTCTCTTGGACTTGTAAC 	
866 866	AGAAAA IGATACAAGAA FRA LIGAAGI IGTO IGTAAAGAACA IGAATGTAATATAGATGA - - - - - - - - - - - - - - - - - - -	
575 938	OGTICACTOGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACT 	

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RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                             Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Henedict,W.F. A method for detecting the predisposition to retinoblastoma and method for detecting a retinoblastoma gene in tumors using a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1981 GATGAATGTAATIGGTGCAGAGAGAGTGCAGTTAGGACTGTTATGAACACTATCCAACAATT
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                                                                                                 AGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAATTCTCTTGGACT 585
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2129 2338	2070 AAMAAATATITIGCAGTATGCTICCACMAGGCCCCCTACCTIGTCACCAATACCTCACAT TITTITITITITITITITITICAGTATGCTTGCACMAGGCCCCCTACCTTG-CACCAATACCTCACAT 2280 AAMAAATATTTTGCAGTATGCTTGCACMAGGCCCCCTACCTTG-CACCAATACCTCACAT	₽ Q
2064 2279	2010 AGAMJAGGAGTATGATTCTATTATAGTATTGTATAAGTGGGTCTTCATGCAGAGAGTGAA 	₽ Çy
2009 2219	1950 AMAGGATACAMGATETTECTEATGETGTTCAGGAGACATTCAAACGTGTTTTGATCAA HILLIHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	ž Š
1949 2159	* 1890 GROTTICCA ROTARGOATA IGCAAAGTGAAGAATATAGACCTTAAATTCAAAATCATTGT 	₽ Q
1889 2099	TB30 GCACACCCTRICAGAATGAGTATGAACTCATGAGAGAGAGAGCATTTTGGACCAAATTATGAT LILILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	FF 99
1829 2039	1770 TTGTGAACGCCTCTGTGTGAGCAGCAGAATTAGAACATATCATCGTGGACCCTTTTCCA 	E 6
1769 1979	1710 CTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACT TITTTTTTTTTATAAAAAAAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACT 1920 CTCTCTTTCACTGTTTTATAAAAAAAGTGTATCGGCTAGCCTATCTCCGGGCTAAATACACT	14 5
1709 1919	TIGEANATGENAGAGACACAAGCAACCTECAGCCTTCCAGACCCAGAAGCCAFTGAAATCTAC 	₽ 8
1649 1859	1590 GTAFCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACGCGTGTAAATTCTAC 	¥ \$
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1529 1739	1470 AGAFTCACCTTFAFTTGAFCTTATTAAACAAFCAAAGGACCGAGAAGGACCAACTGATCA 	¥ 5
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1409 1619	1350 CITTIGAFI FI FANAAAGIGA FCGAAAGI FI FA FCAAAGCAGAAGCAGACTI GACAAGAGA LI HELLI HELLI 1560 CITTIGA FI FITA CAAAGI GA FAGAAG FFFFA FCAAAGCAGAAGGCAGACTI GACAAGAGAG	3d 80
1349 1559	1290 FOTICAETO GGAACAGATITGTOTTTCCCATGGATTCTGAATGTGCTTAATTTAAAAGC HIHHHHH HHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	<u> </u>
1289 1499	1230 TITATTGGGGTGGGGCTCTTGAGGTTGTAATGGGGCACATATAGCAGAAGTACATGTCAGAA HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	₽ Ş
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υğ	459	GACTICCAA
Çy	310	CCAGAAAATAAATCAGATGGTAATGTAACAGCGACCG
υb	519	CONSANATAATCAGATGGTATGTANCAGGACCGTGTGCTCTAAAGANGTGCTG
QУ	70	AAGCAACCTTCCTAAACCACTGAAAAAACTACGCTT
Db	79	V-14-1-1
Qy	2430	AGATGGAAGTAAACATGTCCCAGGAGAGTCCAAATTTCAGCAGAAACTGGCMIAAAT
qq	2639	AGATGGAAGTAAACATCTCCCCAGGAGAGTCCAAATTTCAGCAGAAATTCGGAGAAATGG
Оy	2490	TCTAC1CGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTC
Db	2699	TTCTM:TCGAM:A:\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\
Qy	2550	GGAAGAGAAFGAGGATCICAGGAGACCTTGGTGGACACTGTGTATACACCTGTGTATACT
Db	2759	GEANGAGAAATGAGAGATTTCAGGAGATCTTGGGGGGAAATCATTG
QУ	5	2.
В	2819	TCTCTCACAGATGTGACTGTATAACTTTCCCAGGTTCTGTTTATOO
Qy	O١	TEMPETELLITIESESAIVAVATESES VON CONTRACTORIO EL CONTRACTORIO DE LA CON
Db	∞	TTCAGCTCTTTTGTGGGATATAAAATGTGCAGATGCAATTGTTTGGATGCALGCTAAcc
ОУ	7	100
Дb	9	ACTTGAAATGTTAGTCATTGTTATTTATACAAGATTGAAAATC.11s-161AAA1C-16CCA
Оу	2790	1337
Вb	2999	TTTAAAAAAGTTGTAGCAGATTGTTTCCTCTTTCCAAAGTAAAATTOCTGTGCTTTA
Qу	(J	AGTAAGAATGGCCCTAGAGTGGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTT
Db	3059	AGTAAGAATGGCCCI
Qy	-	TAATTIATATGTATATTTT
Db	3119	ATTAATTTATATGTATAT
Су	2970	-
υþ	3179	TTTAACATGAACACCCTTAGAAAATGTGTCCTATCTATCT
Š	01.01	TGACTGCCCATTCACCAAAATTATCCTGAAACTCTTCTGCAAAAAATGGATATTATT
Db	3239	TTCTGCAAAAATG
Οy	3090	ЛТТАБАААААА П АСТААТТЕГАСАСАН АБАТЕГГАТТЕАТТЕАТТАСТАТЕСБАА ГСТБАТА
Db	3299	ATTAGAAAAAAAATTTACTAATTTTACACATTAGATTTTACTATTGGAATCTGATAT
Cy	_	GIGIGETIGITIIATAAAATITIGETITIAATIAAATAAAAGETEGGAACEAAAGTA
ф	3359	ACTGTGTGCTTGTTTATAAAATTTTGCTTTTAATA
Çγ	bear or	AACCATATGATACTATCATACTACTGAAACAGATTTCATACCTCAGAATGTAAAAA
Db	3419	AACCATATGATACTATCATACTGCTGAAACAGA
ОУ		
!	3270	TACTGATTATTTTCTTCATCCAACCTATGITTTTAAATGACGAGTAITAITGATAGT

OY 690 IGHAACAECTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAGAACTTTA 749 ID 1053 IGHAACAECTAATGGACTTCCAGAGGTTGAAAATCTTTCTAAACGATACGAGAAGAATTTA 1112 OY 758 TCTTAAAAATAAAGATCTAGATCTAGATGAAATCTTTTTTTGATCATGATAAAACTCTTCAGAC 809 IHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	70 ANAACTAGAAAATGATACAANAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATAT 	UY 390 ATTACANATHANANATGATETTATTETTATTTO AGTTAATGETATGIGICCTTGACTA 449 HILLIH OY 510 CALLANGGITGACCTUGAACCCCAUUGGAGGTCAGAACAGGAGTGAGGATACCAAA 569 11111111111111111111111111111111111		PRIECIPES 2007. CONSECURACINE OF MISMACCINES 5. INDEEDS 07 GAP 90 ICCTGAGGTIGGACCTAGANGAGATGTCGTTCACTGTTTTACTGAGCTACAGAAAACATAGA 1 1	2994 bp DNA linear PAT 08-SEP-20 altent US 5998134. 019719 019719 04) 04) 0598134. 08. Fred, No. 0. 1000 DEAR PAT 08-SEP-20 1001 Linear PAT 08-SEP-2
HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Qy		Qy 1350 CTTTGATTTTAATCAAAGTGAACGTTTTTATCAAAGCAAGAGGCAACHIGACAAJAGA 1409 LHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	99 1170 AGAACGAPTALICCATTCAAAATTTTAGCAAACTTELIGAATGACAACATHTTTGALAIGIC 1224 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	WY STO GGTGANTGTANTTCGTCACACACTCCAGTTAGGACTGTTATGANCACTATAGCANATT 929

Ouery Match 76.3%; Score 2534; DB 6; Length 2994; Best Local Similarity 99.8%; Pred. No. 0; Matches 2537; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	rce NT 974 a	Ant Ret Pat	SOURCE Unknown. ORGANISM Unknown. REFERENCE 1 (bases 1 to 2994)	FION Sequence 3	RESULT 13 ARO98189 ARO98189 2994 bb DNA linear PAT 14-FEB-2001	OY 2510 TCTCTCACACATGTGACTGTAT (263) 111111111111111111111111111111111111	Oy 2550 GOAAGAGAAATGAGGTCTGAGGAGCTTGGTGAACACTGGTAGAGAGCTCTGGATTGATT	OY 2490 TICTACTCGAACACGAAGGAAAACGAAAATGAATGAATGATAGAAATAAACAAAAAAA 2549 	QY 2430 AGATGGAAGTAAACATCTGCCAGGAGAGTCCAAATTTGAGCAGAAACTGGCAGAATGAC 2489 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 2370 AAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGATGAGGCCAGATGAAGC 2429 	OY 2319 COMMANATANTOMATOSTATOTAN/ASCGAGGTTTS/TOANAMAASTGCTGAAGG 2369 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	OY 2250 GACTOCAACATOAAGAATOTTAGTATOAATTOGGGAAAGATTOGGGAGAAGIT 2309 	OY 2196 TATTTCACCCCGAAGAGTCCATATAAAATTCAGAAGGTCGGCAACAACACCAACAAAA1 2249 HILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Oy 2139 TCCTCGAAGCCCTTACAAGTTTCCTAGTTCACCCCTTAGGGATTCCTGGAGGGAACATCTA 2189	OY 2070 AACAARIAFEFFIGCAGIAFIGCTERCACCAGGCCCGTACCTEGFIGACGATACCTCACAT 2129 HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	OY 2010 AGAAGAGGAGTATGATTGTATTATAGTATTGTATAACTGGGGGTGAGAGAGA	OY 1950 AACAGCATACAAGGATCTTCCTCATGGTGLLCAGGAGACATTCAAACGTGTTTTGATCAA 2009
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Retinoblastoma fusion proteins Patent: US 6379927-A 3 30-APR-2002:
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             Antelman,D., Gregory,R.J. and Wills,K.N. Tissue specific expression of retinoblastoma protein Patent, IP 2001503638 A 2 21-MAR-2001,
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CC Strandedness: Single:
CC Topology: Linear;
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DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS
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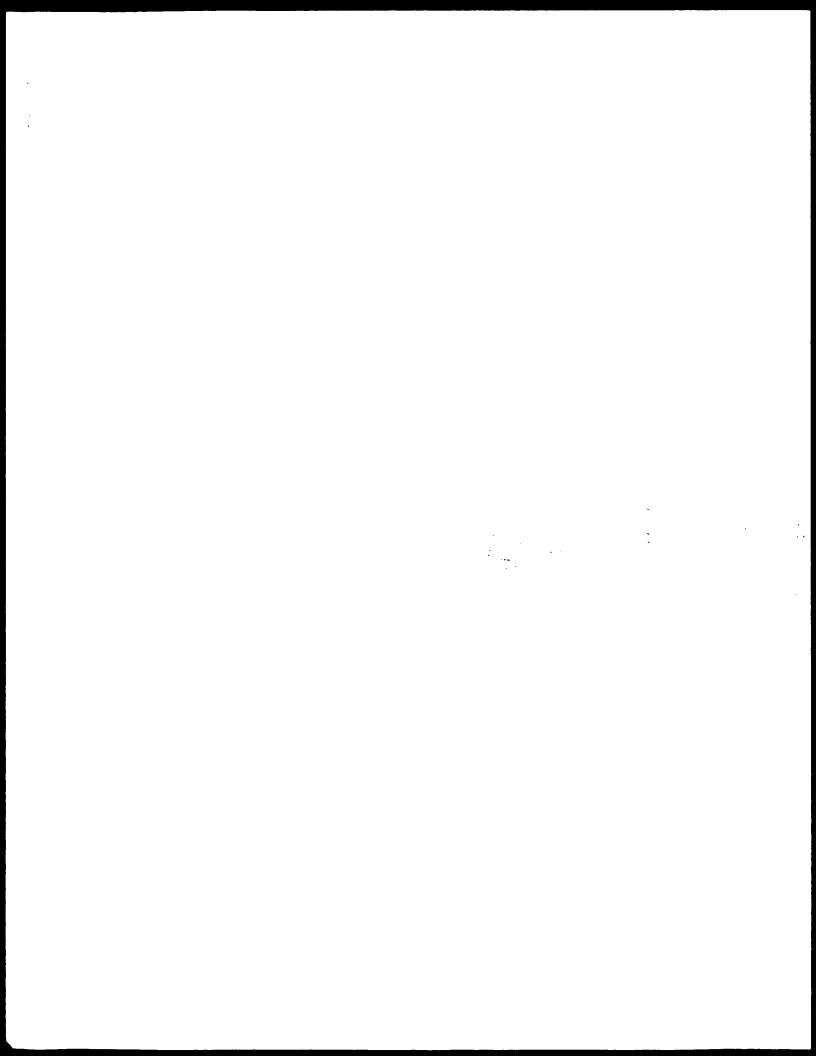
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2973 ICTCTCACACAGATGTGACTGTAL 2994
                2610 FOFO PACAGA FOFGACTIONAL 2631
                                                                  2913 GGAAGAGAATGAGGATCTCAGGACCTTGGTGGACACTGTGTATACACCTCTGGATTCATTG
                                                                                                      2550 GGAAGAAA IGAGGA ICTCAAGAACCTIGGIIGGACACTG I GTACACCICTGGA FIICAYITG - 2609
                                                                                                                                     2853 FITOTACTICGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTICAAACAA
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SUMMARIES

ALLIGNMENTS

311.11	AUTHORS	PRESENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	HUMRHAIRA	RESULT 1
Directions of a DNA sequence in retinoblastomas and mesonchymal	Friend, S.H., Horowitz, J.M., Gerber, M.R., Wang, X.E., Bogenmann, E.,	Mammalia; Primates; Catarrhini; Hominidae; Homo.	Homo sapions	Homo sapiens (clone: p4.7k) cDNA to mkNA.	retinoblastoma protein.	M33647.1 GI:190945	M33647 J02994	Human retinoblastoma associated (kB) mkNA, complete eds.	HUMRBAlkA 4600 bp mena lidear Pki 12 JUL 1995		

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GAACACCACGAAAAAGTAACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACCCCCAG 736
                                                                                                                                                                                                                                                          AAAATCTTTCTAAACGATACGAAGAAGTTTATCTTAAAAATAAAGATCTAGATGCAAGAT 616
                                                                                                                                                                                                                                                                                                             ATTITATACCTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 946
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                                                                                                      LA FERRETGGATGATGA FAAAACTOTTCAGACTGATLCTATAGACAGTITTGAAAACACAGA
                                                                                                                                                      TATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGA 676
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                                                                                                                                                                                                          AAAATCTTTCTAAACGATACGAAGAAATTTTATCTTAAAAAATAAAGATCTAGATGCAAGAT 1006
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SDQPSENLISYFNNCTVNPKESILKRVKDIGYTFKEKFAKAVGQGCVETGSQRYKLGV
RLYYRVMESMLKSEEERLSTONFSKLLNDNIFHMSLLACALEVVMATYSKSTSONLDS
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IPAGNIYISPLKSPYKISEALPTPTKMTPRSPIIVSIAESEGTSEKEQKINQMVCNSD
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SPLFDLIKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFSKLERTCELIYLTQPSSSISTEINSALVLKVSWITFLLAKGEVLQMEDDLVISFQL
MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPRPPRRGONRSARIAKQLENDYRIIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MPPKTPRKTAATAAAAAAEPPAPPPPPPPPPEDPEGDSGPEDLPL
VRLEFEETEEPDFTALCQKLKIPDHVRERAWLTWEKVSSVDGVLGGYIQKKKELWGIC
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/db_xref="GI:190946"
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/db xrof="taxon-9606"
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                                                                                                                                                    TGAGAGAGACAGGCATTTGGACCAAATTATGATSTGTTCCATGTATGGCATATGCAAAGTSA
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                                                                                                                           TGAGAGACAGGCATTTGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA
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                                                                      AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCATACAAGGATC110010A110113
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Molecular mechanisms of oncogenic mutations in tumors from patients with bilateral and unilateral retinoblastom
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1352. .1375
   resulting in premature stop; Associated with this mutation is a large 13g14.3 sub-band deletion; G00:118-734" /citation=[5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Tumor GOS159 unilateral mutation causing a
premature stop; GOO-118-734"
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                                                                                              /note-"Tumor GOS13 unilateral frameshift mutation
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                                                                                           1681 CATGGALTCTGAATGTGCTTAATTTAAAAAGCCTTTGAATTTTTACAAAGTGALCGAAAGTL 174
                                                                                                                                                  1157 CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTACAAAGTGATCGAAAGTT 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             617 TATITITGGATCATGATAAAACTCTTCAGACTGATTCTATAGACAGTTITGAAACACAGA + 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              557 AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGAI 616
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2356 2880	CCAAATTTCAS AAACTGGAAAATGAATTGTACTCGAACACGAATGCAAAAGAAGAAGCAGA 	2297 2821	5 & 6
2296 2820	TACCETTEGATATTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGAGT 	2237	DP OY
2236 2760`	GCGACCGTGTGCTCAAAACAAGTSCTGAAGGAAGGAACCCTCCTAAACCACTGAAAAAAC	2177	4d 6A
	TTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAAT	2117 2641	ê k
2116 2640	PEPEVAGAAGGIO IGCCAACAGCAACAAAAATGACTCCAAGATCAAGAATCTTAGTATCAA 	2057 2581	qq Yo
	CMCCTTACGGAFTCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAA	1997 2521	Ê ç
	GCCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTT	1937 2461	ê ç
1936 2460	TCTATAACTCGGTCTTCATGCAGAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCA	1877 2401	ρ. Υο
	TTCAGGAGACATTCAAACGTGTTTTGATCAAAGAAGAGAGGAGTATGATTCTATTATAGTAT	1817 2341	eg Cy
1816 2340	AGANTATAGACCETAAATECAAAATCATEGTAACAGCATACAAGGATCTTCCTCATGCTG	1757 2281	9 4g
	697 "IGAGAGA"AKKCAPTERGANGAAAFFA IGAFGTGTECCAPGTATGGCATATGGAAAGTGA 179 	1697 2221	ê å
	ANTENIAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGACTATGAACTCA	1647 2141	ê ê
	ATCGG*TAGC*TATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTCTG	1577 2101	ê ç
1576 2100	CCTTCCAGACCCAGAGCCATTGAAATGTACCTCTCTTGACTGTTTATAAAAAAGTGT	1517 2041	Db.
	AAAAAGGTTCAACTACGGGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAAG	1457 1981	£ ç
1456 1980	CTCTCCMBAATAATCACACTGCABCABATATGTATCTTCTCCTGTAAGATCTGCAAAGA 	1397 1921	ş ç
1396 1920	AARCAAAGGACCGAGAAGGACCGACCGACCGAGACCGAGCTGGATCTGCTCTTTTAATCTTCCTCTTTTAATCTTCCTCTAATCTTCAATCAAAGGACCGAGAAGAAGAACCAACTGATCACCTTGAATCTGCTCTTTAATCTTC	1847	οφ γο
1336 1860	ATCHANTCATGRATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAAC	1277 1801	£ 5
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	Unknown. W Unknown. Unclassified.	ORGANIS!	Š
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	AA.	9.9	40
	TTTTTAAATGAGGATTATTGATAGI 3161	3137	Qy
46 ,6,0	AGATTTCATACCTCAGAATGIAAAAGAACIIACIGAIIAIIIICIICAFCAAC	3601	Db
3] 44.	CAGATTTGATI ACCTCAGAATGTAAAAGGAACTTACTGATTATTTTTTTTT	3077	γ0
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3076	TTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATATGATACTATCATACTAC	3017	45
55.4U	TTTACTATTGCAATCTGATATACTGTGTGTGTTTTA	3481	40
3016	AGATTTTATTTTACTATTIGGAATCTGATATACTGTGTGTGTGTTTTATAAAATTTTTCT	- 6	ζ.
4 8 0	AACTCTTCTGCAAAAATGGATATTATTAGAAAATTAGAAAAAAATTACTAATTTTACAAAT	3421	덩
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34.20	GIGICCTATCIAICTTCCAAAIGCAATTGATTGACTGCCALICATCAAAAITAICTIG	3361	90
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28.85	TARABAT FEARACACARABAT TELETERALETARCALCACACACACACACAT I ACAAAAT	2777	QΥ
* 400	GATAACCAAGGCTGTCTGACTACTTTGCCTTCTTTTGTAGCATATAGGTGATGTTTGCT	3241	마
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	TTCCAAACTACAAATTCCTGTGCTTTATGCATAGTAAGAATGCCCTAGACCGCAACTACT	3181	40
2716	ATGGATAGTAAGAATGGCCCTAGAGTGGGAGTCCT	2657	Qγ
4187	CTGCCATTTAAAAAGTTGLAGCAGATTGLLTCCTC	3121	da
2634	AAGATTGAAAATCTTGTGTAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTT	2597	Vγ
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2596	AGATGCAA FTG1FTFGGGTGATTCCTAAGCCACTTGAAATGTTAGTCATTG1TATTATTATA	2537	ОУ
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	CA 1036 [] CA 1105	7. GAGTAATGGAATGCATGCTTAAATCAGAAGAAGAAGAAGAAGATTATCAAAATTTTAGC 	ФУ 977 Db 1046	
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	GA 576 GA 745	7 TATITITGRATOATRATAAAACTCITCAGACTGAITCTATAGACACAGTTTTRAAACACAG 	Ωy 617 Db 686	- 0
	6 6	7 AAAATCITTICTAAACGATACGAAGAAATTTTATCTTAAAAATAAAGATCTAGATGCAAGAT 	Oy 557 Db 626	- 0
	ത ഗ	7 AFFITATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG	Oy 497 Db 566	- 0
	AA 565	7 AAGTICTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAA/ 	Qy 437 Db 506	
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               Xu,H. J., Hu,S.-X. and Benedict,W.F. Broad spectrum tumor suppressor genes gene products and methods tumor suppressor gene therapy Patent: US 5912286 A 2 15 JUN 1999;
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                                                    CATGGATTCTGAATGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTT 1210
                                                                                                                                                                                                                        TGGGCACATATAGCAGAAGTACATCTCAGAATCTTGALTCTGGAACAGATTTGTCTTTCC 11%
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Xu,H.-J., Hu,S.-X. and Benedict,W.F.
Broad-spectrum tumor suppressor genes,
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Human DNA in the diagnosis of retinoblastoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SHOHIDA
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Molecular mechanism of retinoblastoma gene inactivation retinoblastoma cell line Y79
                                                                                                                          Lee,E.Y., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M. 1.
                                                                                                                                                                                                                                                                                                           Science
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                                                                                                                                                                                                                                                                                                                                                                 Human retinoblastoma susceptibility gene: cloning, identification and secure week secure week to be susceptibility of the content of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 243 to 4740)
Lee,W.H., Hookstein,R., Hong,F., Young,L.J.,
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Homo sapiens (clone: RB-[1,5]) foctus retina cDNA to mkNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human retinoblastoma susceptibility mRNA, complete cds
                                                                                                                                                                                                                     3823889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
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                                                                                      Lee, W.H.
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                                                                                      TATETETEGATICATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACAGAGA 676
                                                                                                                                           AAAATCTTTCTAAACGATACGAAGAAAATTTATCTTAAAAAATAAAGAT 11AGATCGAAGAT 1141
                                                                                                                                                                                                                                                                                                  ATTITATACCTTTTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTG 556
                                                                                                                                                                                                                                                                                                                                                     ADGITICICIGITANAGAACATGAATGIAATATAGATGAGGIGAAAAATGITITATITCAAAA 1021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038 bp upstream of EcoRI site; chromosome 13q14.1-q14.2.
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1757 AGAATATAGACCTTAAATTCAAAATCATTGTAACAGCAIACAAGGAICTICCTCAIGCIG 1816
                                                     1337 AATCAAAGGACCGAGAAGGAQCAACIGAICACCIIGAAICIGCIIGIIGCICIIAAICIIC 1396
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2837 GIGTOCIAICTATCTTCCAAATGCAATTTGATTGACTGCCCATTCACCAAAATTATCCTC 2896
                                                                                                                                                                                                                                                                                                                                     3122 CANGATTGANAATCTTGTGTAANTCCTGCCATTTAAAANGTTGTAGCAGATTGTTTCCTC 3181
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                                               4302 CITGITITATIAAITTATATATGIATATITITIAAITTAACATGAACACCCTTAGAAAAT 3361
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                                                                                            CHGTTTTATTAATTTATATGLATATTTTTAATTTAACATGAACACCCTTAGAAAAT
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636 AACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAGAACACCAGGAAAAAAGTAA
                                           949 CGAAGAAATTTATCTTAAAAAATAAAGATCTAGATGCAAGATTATTTTTTGCATCATGATAA 1000
                                                                                     576 CGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTTGGATCATGATAA 6×5
                                                                                                                                                                          516 TECTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAATCTTTCTAAACGATA 579
                                                                                                                                                                                                                                                                456 TGAATGTAATAGATGAGGTGAAAAATGTTTATTTCAAAAAATTTTATACCTTTTATGAA 515
                                                                                                                                                                                                                                                                                                                                   709 AGCTGTTATACCCATTAATGGTTCACCTCGAAAACCCCAGNCGGGTCAGAACAGGAGISC 768
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                                                                                                                               TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAA 888
                                                                                                                                                                                                                                                                                                            ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAATTCTCTGTAAAGAACA 828
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACACGAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retinoblastoma gene probe
Patent: EF 0293266 A 1 30-NOV-10
RESEARCH DEVELOPMENT FORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 4580)
Forgy K T , T'Ang,A., Mulphree,i..A. and Benedict,W.F.
A method for detecting the predisposition to retinoblastoma and
method for detecting a retinoblastoma gene in tumors using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.sapiens DNA for 4.6 kb retinoblastoma gene probe-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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99.48;
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2/96 AIGTATATTTTAATTTAACATGAACAGCCTTAGAAAAGTGTGCCTATCTAT	υb		1716 CCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATT 1775
95 ACHACHERSCHICHERMASARARAGA GARRERGER GERERGER AND HAZIRARERA 97 ACHACHERGCENCETTGEAGCATATAGGEGATGETTOCHCHGERTETTATTATTATTATTATTATTATTATTATTATTATTATT	dd dd		1656 GARGOTTTTOCARGACAGCCTGCAGAAATGAGTATGAACTCATGAGAGAGAGA
TIGOTTTA (RGATA) AAGAATGGGCCTA (AGAGTGGGAGTCCTGATA) AACCCAGGGCCTGTGTG THELLITTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	da VQ		1596 GCTAAATACACTETGTGAACGCCTTCTGTCTGAGCACCACAATTAGAACATATCATCTG 1655
TAAATCCTGCCATTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCAAGTAAAGTAAAATTGTTGTTGTAAAATCAAAGTAAAAATCGTTGTAGCAAAGTAAAAAAGTAGTTGTTGTTGTTCCAAAGTAAAAAATCGTTGTTGTAAAAAGTAAAAAAAGTAGTAGTAGTAGTAGTA	Qy Db		1546 ATTGAAATCTACCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCCG 1595
GATTCCT GATTCCT	Db Vy		1476 TGTAAATTCTACTGCAAATGCAGAGAGAGACACACATCAGCCTTCAGCCTTCCAGACCCAGAAGCC 1535
2496 ACATTIAATATCTTCAGCTCTTTTTGTGGATATAAAATGTGCAGAGGCAATGGTTATTTTTTGTGGATATAAAATGTGCAGAGGCAATGGTTGTTGTGGATATAAAAATGTGCAGAGTGGCAATGGTTGAGTTGTTGTGGATATAAAAATGTGCAGAGGCAATGGTTGTTGAGTTGTTGTGGATAGAAAATGTGCAGAGTGGCAATGGTTGAGTTGTTGAGTTAATAGAATGTGCAGAATGGCAGAGTGGAATGGTTGAGTTAATAGATAG	υb		1416 TGCAGCAGATAIGIAICTEICTECTECTGTAAGATCICCAAAGAAAAAAGGTTCAACTACGCG 1475
CTGGATT	Оу		1456 ACCAACTGATCACCTTGAATCTGCTTGTCTCTTAATCTTCCTCCAGAATAATCACAC 1415
2376 TACCTCAAACAAGGAAGAGAAATGAGGATCTCAGGACCTTCSTGACACTGTGTGACACTGTGTACACCT 2435 	ob Vy		
2316 GCCAGAAATGACTITCTACTCCAACACGAATGCAAAAGCACAAAATGAATGATATATA 2379 	dd. Ao		1236 CTTGACAAGAGAAAGATAAAACAFITAGAACGAFGTGAACAFGGAATCATGGAATCCCT 1295
ATCAGA IGAAGCACATGGAAGTAAACATGTCCCAGGAGACTCCAAATTCAGTAGAAACT 	, pb		1176 TAATTTAAAAAGCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAA 1235
	da Yû		1116 TACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCT 1175
"TICTGAGAAGTTCCAGAAAATAARTCAGATGGTATGTAACACCACCATCCTGTGTGTAAAAATTAACTTTTTTTT	. da	-	1056 TETTOATATUR OTETATURRIGIGRUGUSTIRGAGGTIGIAATGGSSCASTATAGSGAGAG 1115
ACCAACCAAAATGACTOCAAGATCAAGATCTTACTATTATTATTATTATATTA	Оу Db		996 TAAATCAGAAGAAGAACGAITATCCATTCAAAATTTTAGCAAAGTTCTGAATGACAACAT 1055
AGGGAACATCTATATTCACCCCGGAAGAGCCATATAAAATHCAGAAGAGCGCAAC	לט לע		946 TGGATCACAGAGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCT 995
ANTACCHCACATROCICGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGG TETTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Фу Ръ		876 TATAGGALAGA KETTIAAAGAAGTAAGATTTGCTAAAGCTGTGGGGACAGGGTTGTGTCGAAAT 935
-1896 GCAGAGACTGAAAACAAATATTTTGCAGTATGCTTTCCACCAGGCCCCCTACCTTCTCACC 1988 ITTITITITITITITITITITITITITITITITITIT	dd An		816 TTOTTATTTTAACAACTGCACAGTGAATGCCAAAAGAAAAG
	qq		756 TATOUAACAATTAATGATGATTTTAAATTGAGGAAGTGATGATGAGGATAATCTGAT 815
CAAAATCATTOTAANAGCATACAAGGATCTTCTTCTGTGTGTTGTTCATGAGAGATTCAAAATCATTTCAAGAGATCTTCTTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	ob V		696 CCLIGA IGAAGAGGIGAALGIAAL ICCTCCACACACACICCAGTIAGGACTGTTATGAACAC 755 1059 CCTTGATGAAGAGGTGAATGTAATTCCTCCACACACACTCCAGTTAGGACTGTTATGAACAC 1128
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TITLE
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Matches 2142; Conserv
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                                                                        TATTTTTGGATCATGATAAAACTCTTCAGACTGAFTCTATAGACAGTTTTGAAACACAGA 676
                                                                                                                                                        AMANTOTTTOTAANOGATACGANGAAATTTATCTTAANAATAANGATCTAGATGCAAGAT
                                                                                                                                                                                                                            AAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAATAAAGATCTAGATGCAAGAT 616
                                                                                                                                                                                                                                                                                                        ATTITATACCTTITATGAATICICITGGACTTGTAACATCTAATGGACTTCCAGAGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGTICTCTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTG 961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retinoblastoma gene-cancer suppressor and regulator Patent: US 5998134-\lambda 4 07-DEC 1999,
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Lee, W.-H. and Lee, E.Y.-H.P.
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                                                                                                                                                                                                                                                                      Matches 2142; Conservative
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Best Local Similarity 99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2762 TACGCTTIGATATTGAAGGATCAGATGAAGCAGATGJAAGTAAACATCTCCCAGGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2417 GTGGACACTGTGCACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAT 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2297 - CCAAATTTCAGCAGAAAATTGGCAGAAATGACTTCTAFTFGAACACGAAATGCAAAAGCAGA - 2354
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    4.5
                                                                                                                                                                                         377 GAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAAATTATTG 436
                                                                                                                                                                                                                                317 TTAFTGGAGGAGTIGACGTAGGTGTTATAGGCATTAATGGTTFGAGTFGAAGAGGAGGAGGGAGGGAGG
ATTITATAGOTTITTATGAATTOTTIGGAGTTGTAAGAAGAAGTTGGAGAGTTGGSTA
                                  AAGTTCTCTGTAAAGAASAIGAATGTAATAGATGAGGTGAAAAATGTTTATTTCAAAA 496
                                                                                                                 GAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAAAAATJATACAAAAATTATTG 961
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OS Unide
PN JP 20
PD 21-MA
PF 13-NO
PR 15-NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antelman,D., Gregory,R.J. and Wills,K.N.
Tissue specific expression of retinoblastoma protein
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13-NOV-1997 JP 1998522958
15-NOV-1996 US 08/7515
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JP 2001503638-A/2
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                                                                                                                                                                                                                                                                                                                                                                   /db_xre1-"taxon:32644"
6:8 c 593 q 8
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    Mismatches

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7 43	577 ALCOCCTATCTCCOCCIAAATACACTTCTGAAACACTCTCCGACTAACAC 	
1576 2101	Qy 1517 CCTFCCAGAGCCAGAAGCCATTGAAATCTACCTCTTTCACTGTTTTATAAAAAAAGTGT 	
1516 2941	457 AAAAAGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCAACCTCAG 	
1456 1981		
1396 1921	Uy 1347 AA1CAAAGGACCAAGAAGCACAACTGATCACCITGAATCIGCTGIGCTG	
1336 1861		
1276 1801	OY 1217 FRANCAAGCAGAAGCAACHIGACAAGAGAATGATAAAACATIIBAGAAGAGGAIGIIGAAC HILLIH HI	
1216 1741	157 CAIGGAIPCEGAAUGEGCTTAAFTTAAAAGCCTTTEGATTTETACAAAGTGAFGAAGCT 	
1156 1681	97 TOGCCACATATAGCANAANTANATOTOANAATOTOSAITOTSGAACAGATTTGTCTTTCC 	
1096 1621	OY 1037 AACTICIGAATGACAACATTUTICATATGCOTTTATTGGCGTGGGCTCTTGAGGGTGTGTAA	
1936 1561	OY 977 GAGIAA IGGAATO ATROCTTAAA TO AGAAGAAGAAGAATTA IGGATTA IGGAATTTTTAAGA 	
976 1501	17 GANAGGETTGTGTGAAATTGGATTGGATGGATGGAAGTTGGAGTTGGTTTTTATG 	
916 1441	OY 857 TACTIGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAGAAATTTIGCTAAAGGTGTGG 	
856 1381	97 AAGCITCAGAAAAKCIGATTTCCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG	
796 1321	CY 737 TTANGACTGTTATGAACACTATICCAACAATTAATGATGATTTTAAATTCAGCAAGTGATC HHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
736 1261	cy 677 gaacaccacgaaaagtaaccttgatgaagagtgaatgtaattgctgcacacaca	
676 1201	UY 617 IAFTETTGEATGATGATAAAACTCTTCAGACGCTGATTCTATAGACAGTTTTGAAACACAGA	
616 1141	57 AAAATCITICTAAACGATACGAAGAAATITATCITAAAAATAAAGATCIAGATGCAAGAT 	
1081	DE 1022 ALL CTALACCLITTATGAATTCTCTCTGGACTTGTAACATCTAATGGACTTGCAGAGGTYG	

ad Vy	Üy Db	4a 45	Оу	Db Db	qa Að	Oy Dh	Qy Db	qa 	qq ; Ao	d d	det Að	Qy Db	. Db	dci
241	235	181 181 191	223 276	217	211 264	205 258	199 252	193 246	187 240	181 234	175 228	169 222	у 1637 b 2162	210
7 GEGGACACEGEGTACACCCCCIGGATECACIGTCICACAGATGIGACIGIA 2459 	7 AAATGAATGATAGCATGGATACCTCAAACAAGGAAGAGAAATCAGGATCTCAAGGCCTTG 243F 	7 CCAAATITCAGCAGAAACTGGCAGAAAIGANITCIACIGGAACAGGAAIGAAAGGAAGA 2356 	7 TACGCTTTIGATATTTGAAGGATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGGAGGAGGT 	7. GERAR CERTGEGET CAAAAGAAGTAGT GAAAGGAAGGAAGGAAAGCACCT GEAAAAGAACAACCACT GAAAAAAAAAA. 22.46 	7 TTGGTGAATCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAAT	7	7 CACCCTIACEGAI ICCIGGAGGGAACATCIAIAI LICACCCCTGAAGAGTCCATAIAAA 256 		7 TCTATAACTCGGTCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGC11C7ACCA 1946 	ITGATCAAAGAAGAGGAGI - - - - - - - - - - - -	7 AGAATATAGAGCCITAAATTCAAAATCATTGTAACAGCATACAAGGATCTTCCTCATGCTG 1816 HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI		7 AATTAGAACATATCATCTGGACCCTTTTCCAGCACCCTGCAGAAGGAGTATGAAYTGA 16 A 16 A 11 H H H H H H H H H H H H H H H H H	2 ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTGTGTG

Search completed: January 17, 2003, 18:10:32 Job time: 5279.71 sees

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Command line parameters:

MODEL-Irame-p20.model -DEV-xlh
-O_FG02_[708FT_Spec] (USE-025459/FED31_15012033_152137_24309/AFF_3ubfy.Lasta_1.13467
-O_FG02_[708FT_Spec] (USE-025459 -FINALTCH-0.1 -LOOPCL-0 -LOOPEXT-0
-DH-GenEmb1 -OFWT-fastap -SUFFIX-rge -MINMAICH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -STAW1-1 -END--1 -MARRIX-blosum62 -TWANS-buman40.cd1 -LIST+45
-DOCALIGN-200 -THE_SCOME-pcf -THE_MAX-100 -THE_MIN-0 -AIGN-15 -MODE-LOCAL
-OUTEMT-plo -NORM-ext -HEARSIZE-500 -MINLEN-20000000000
-USEP-INSOUD5454 -MONE-EXTAM-12660 -FUADAL_1601203_15213_23309 -NOED-6 -TCEU-3
-NO_XLEXY -NO_MAN--INGEDEPY -NOED-6 -WAITH-1-ONGEO-FUADAL-17-0
-WARM_FIMEOUT-40 -THEARS-1 -XJAPOP-10 -XJAPEXI-0.5 -FGAPOP-6 -FGAPEXT-7
-WARM_FIMEOUT-40 -THEARS-1 -XJAPOP-10 -XJAPEXI-0.5 -FGAPOP-6 -FGAPEXT-7
-WARM_FIMEOUT-50 - STAM-50 - STAM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               total number of hits satisfying chosen parameters:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Listing first 45 summaries
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em_htgo_other:*	em_}t.go mus:*	em_ht qo., hum: *	em_sy:*	em_ht q_vrt:*	om_htq_mam:*	em_htq_rod:*	om_htg_pln:*	em_htq_mus:*	em_htq_other:*	em_htq_inv:*	em_htq_hum:*	Offic V1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	SOURCE Unknown. ORGANISM Unknown. Unclassified. 2994) AUTHORS Antelman, D., Gregory, R.J. and Wills, K.N. HILE Rethroblastoma fusion polypeptides JURNAL Patent. CD: 6074850 A 3 14 JUN 2000; FEATURES Location/Qualifiers SOURCE //ORGANISM="Unknown" HASE COUNT 974 a 618 c 593 q 809 t	REFERENCE AUTHOR REFERENCE AUTHOR 1111.E 3-UGHA FEATURES FEATURES GORIGIN
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•	qq	1159	ATAGACAGTTTTGAAAC	121н
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Tissue specific expression of retinoblastoma protein
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	269	y 250 ThrileGinGlnLeuMetMetIleLeuAsnserAlaserAspGlnPreserGluAsnLeu 	£ 99
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Bookstein,R. and Lee,E.Y.
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Homo sapiens (clone: p4.7k) cDNA to mRNA.
                                                                                                                                                                                                                                                                        Draft entry and computer-roadable copy of sequence for [1] kindly provided by S.H.Friend, 10-FEB-1988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Friend, S.H., Horowitz, J.M., Gerber, M.R., Wang, X.F., Bogenmann, E.Li, F.P., and Weinberg, R.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                 364 CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAAGAAATTGATACC
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/db_xre1="GI:190946"
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/note-"retinoblastoma-associated protein"
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429	nLouThrArgGluMetTleTysHisLeuGluArgCysGluHi	_	
	CulysAlaFheAspEhcT,£L;SVallleGluSerFheIleLysAlaGluGly 	390 1564	
	rThrSerdInAsnLeuAspSerdIyThrAspLeuSerPheProTrpT] 	370 1504	
369 1503	ICHISMETSETLEULEUA aCysalai.eug uvaivalmeta ia 	-A-	
349 1443	@ludluarqfəuSerlle@lnasnPheSerLysLeuLeuAsnAsp - - - - - - - - - - - - - - - - - - -	330 1384	
329 1383	YSO211 BA19TY rLYSLOWY YV 1 A19LOUTY FTY RAEGVALMO! 	310 1324	
309 1323	leClyfyflePhelysClulysPheAlalysAlavalClyClr 	290 1264	
289 1263	erTyrPheAsnAsnCysThrValAssPrcLysGluSerIleLe: 	27 <u>0</u> 1204	
269 1203	leGlmSlnLeuMetMet.leLeuAsnSerAlaSerAspGlnProSerGluAsr 	250 1144	
249 1143	ASDI CDASPOLUG DUVALASDVALLI CPTOPTOHISTHTPTOVA LATGTHTVA LMCTASD 	230 1084	
	nrlænglothrAspSerfleAspSerFheGlothrGloArg - - - - - - - - - - - - - - - - - - -	210 1024	
	Typtlatlatlatletyflealyfasilysaspleaaspalaargleapledeaaspliisasp 	190 964	
96	AssSert.cuGlyt.cuValThrSerAssglyt.cuProGlyValGlyAssic.cuSert.ysArg	170 904	
	HicclucysAspIleAspCluvalLysAspvalTyrFhoLysAspFhcIleFrsFheMet	150 844	
149 843	AlaArqIleAlaLysGlnLeuGluAsnAspThrArqIleIleGluValLeuCysLysGlu 	130 784	
12	Alaval HeprolleasnelySerproargThrproargargGlyGlhasnargSer 	111 724	
- 4	TGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAA	664	
_		110	
U,	GCTAAAAGGGGAAGTTATTAGAAATGGGAAGATGATCTQGGTGATTTAGTTTAG	110 604	
0.	ATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA	544	
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2644 6	y 730 P	710 T 2524 A	όу 690 Th Db 2464 AC	70 G	50 P	630 2284	610 A 2224 C	590 2164	70 A	50 T	530 A	10 P	1864 C	70 T	50 G	430 I 1684 C	Db 1624 A
	rgSerAlaGluGlySerAsnProE 	hrSerGluLysPhcGluLysIleAs 	rProThrLysMetThrProArgSe 	lyGlyAscileTyrileSerProLe -	TOTTEPTOHÍSTIEPTOATGSETPT 	Thraspile - - - - - ACAAATATTT	.rqValleuIleLysOluGluGluGluTy 	ThralaTyr ACAGCATAC	<pre>spCln!!cMctMetCy </pre>	rpThrLeuPheGlnHisThrLeuGl 	rgi.euasnihri.euCysGluArgi 	rolestysSerThrSerLeu 	.rgValAsnSerThrAlaAsnAlaG 	hralaalaaspMetTyrLeu 	lyProThraspHisLeuGluSerA 	.euAlaTrpLeuSerAspSerProLe 	ACTIGAÇAAGAGAAATGATAAAAAA
SHISLEUPTECTYCTUSCTTYSPhed	©LysProLenLysLysLenArqPheA { TAAACCACTGAAAAAACTACCCTTTG	nGlaMetValCysAsnSerAspArgVa 	PAGAATCTTAGTATCAATTGGTGAU	@LysSerProTyrL/slieSerGh 	OTYTLYSPheProSerSerProLet 	TyralaSerlbrargProPro 	TASPSerIleTleValEbeTyrAsi 	SASpleuProHisAlaValGlnGli 	TG1y11cCystysV31tysAstileA - - - - - - - - - - - - - - - - - - -	nAsnGluTyrGluLeuMetArqAsp/ 	uLeuSerGluHisProGluLeuGluI 	uPhcTyrtystysValTyrAr 	uThrGlnAlaThrSerAlaPh 	oValArgSerProLysLysI 	aCysProLeuAsnLeuBrolæ 	uPheAspLeuIleLysGlnSe 	HITTERGAACGATGEGAACAECGAATGAII
and trive 76 a	pIleGlu 7 A GAA 2	eulys 72 CAAA 25	AFRICAGE	COOLD C	gliebro 669 - - - - 	7 VOLSLIN 111111 9 VOSBOLP	3310150 21 - 1.111 - 4.415be 61	TPhotys 5	VVVI IIII	Hister 	SHOTIS 4.	yrt.cu ATCTC	luLys Hill AGAAC	hrilm de Hilli MIACG le	STUBLES AF	raGlu 4 HHHH SAGAA 1	GGAATOC 1683

	Db 558 AGTATGAAAGTTGATAATGATGATGAGAAGAAGTGTTGAAGAA	TIO		1b 4 (8 ATCTGTATECTATECTAGETGACCTAGATGAGATGTCGTTCACTTTTACTGAGCTA 497	vy 101 HerystlePhelleAlaAlaValAspl.cu	UY 81 VALSAKSARVATASPALYVALLANGIYSIYTYTI ASIDEYSIYSIYSISINLANTTYDIY 100 	TIO TOTO ANAMATTA ANAMATAN CANATCATOTO ANAMAGANAGO TENGTHANG TENGGANAAA	61 CysGluLysLouLysTicProAspHisValArqGluArqAlaTrpLouThrTrpGluLys	11111111111111111111111111111111111111		QY 21 ProAlaProProProProProProBroInGluAspProGluGlnAspSerGlyProGlu 111111111111111111111111111111111111	OY I MOUPTOPTOLYSTEPTOATYCYSTERATAATATTATAATAATAATAATAATAATAATAATAATAA	09-026	ery March 98 188	9.140-289 Lenath: 4068.50 Malches: ty: 85.88% Conservative: arity: 85.88% Mismatches:	ent Scores:	BASE COUNT 1544 a 902 c 880 q 1524 t ORIGIN	SOUTCO 14839 SOUTCO /Organism Homo supiens*	۲	TITLE Cancer gene determination and therapeutic screening using signature grow sets		Eukalyora; Merazoa; (nordata; Craniata; Vertebrata; Euteleostomi; Mimmalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.	NISM Homo sapiens		AX330701 AX330701.1 GI:18103679	DEFINITION Sequence 1210 from Patent Will546.25.	AX (4070)	Db 2764 GATACCTCAAACAAAGAAAGAAAA 2787	Qy 790 AspThrSerAentlyStItutionlys 797	Db 2704 CTGREAGAAFGAACTECTACTCGAACACGAATGCAAAAGCAGAAAATGAATGATAGCATG 2763
ОУ	qq	Qy	- Db	OV DB	- Oy	Db	Vγ	dd	Db	· oy	, pb	- de		4a .fc	D).	Db	VΨ	Qy Db	Db	Qy	lob	Фу	. Db	ОУ	Db	γυ	del	Qy	Db	Ųγ
390 LeuAsnLeuLysAlaFheAspPheTyrLysVallTedTuSerPheTleTysAiaGiuGly 40	AGAATCTIGATICTGGAACAGATTIGTCTTTCCCATGGATTCTGTATTTTT	∃inAsnLeuAspSerGlyThrAspLeuSerFh⊬FroTrp∃leLeuAsnVa	ATTITUTE THE THE THE TRANSPORT OF THE PROPERTY OF THE THE THE TRANSPORT OF THE	10A BARTSETTETTETTÄ 100 ATTATATATIONA AARSTATTIA 100 AARSTATTIA 100 AARSTATTIA 100 AARSTATTIA 100 AARSTATTIA 1	LeulysSerGluGluGluArgLeuSerTFeGlnAsnPheSertlysLeuLeuAsnAsp 1111411111111111111111111111111111111		310 IleGlySerGlnArqTyrLySLeuGlyValArqLeuTyrTyrArqValMetGluSerMet 3	290 ASPITEGTYTYLLEPHELYSGTULYSPHEATALYSATAVa[6] yShellyffyddiai ens HLLDH HILLHHILLHHILLHHILLHHILLHHILLHHILL	ATTCCTATTTAACAACTGCACAGTGAAACAAAAAAAAAA	270 HeSerTyrPheAsnAsnCysThrValAsnFroLysChuSertHetzuLysArqVattys 289	250 ThrilleGinGinLeuMeiMetHell-ulAsqSerAlaSerAspGinProSerGinAsqLon 269 []	ACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTCTTATTATTTTTTT	AsnLeuAspGluGluValAsnValIleProProHisThrProValArqThrValMetAsn	210 TysTbriogdidThraspSeriTeaspSeriThedTuthroThardThradadtyster 2 [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	140 TyrfluflatteTyrfeutysAsstysAsstewAspAlaA:gLeutLeleuAspHiaAs; 209 	TTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTC	170 AsnSerLeuGlyLeuVallhrSerAsnGlyLeuProGlyValGloAsnLeuSerLysArg	150 HisCluCysasnileaspCluVallysAsnValTyrPhetysAsnPhetleProPheMet 169 	GCACGGATAGCAAAACAACTAGAAAATGATACAA	130 AlaArqIleAlaLysGluLeuGluAsnAspThrArqIleHeGluValLeu*ysGlysGlu	858 ACAGCIGITATACCALIAATGGTTCACCCGGAACACCCACCGACGCAACACACACAC	HePro HeAspolySerProArqThrProArqArqOlyShrAss	798 TGTGTCCTTGACIATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAAAACCATATAAA #57	119	738 GCTAAAGGGGAAGTATIACAAATGGAAGAGATGATCGGTGATTTCATTTC	110	678 ЖИЛТСТАСТСАААГАААТТСТЭСГАЛЬЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭЭ	110	616 CTCTCAGCAAAIGGAAAAGACAACHAAAAHAAAHAAAAAAAAAA	110

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Ph: 416 813-5868
FAX: 416 813-4989
                                     Canada
                                                                             Hospital for Sick Children 555 Univ. Ave.
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CMCtMctC	PheGlnF Tocado	aThrLeuC ACACTTT	sSerThrs AFCTACCT	nSerThrAl TicTACTGC	aAspMetT AGATATGT	TASPHISLE TGATCACCT	pLeuSerAs GCTCTCAGA	rArgGluMet AAGAGAAATG	ulysalaPb AAAAGCCTT	rClnAssl TCAGAATC	SMetSerL	GluGluG HIIIII GAAGAAG	rCinArgT AcAGCGAT	YTYrIleI ATACAFÇI	TPPTAACA	lnGln1.euM \ACAATTAA	pGluGluVa TGAAGAGG	TCAGACTG
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AR144797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 480)
Loo,E Y , Bookstein
Draft outry and computer-readable copy of sequence in [1] kindry provided by 8.Hookstein, 27-APR-1987.
                                                                                                                                                                                                 88320373
                                                                                                                                                                                                                                                                                                                                 retinoblastoma cell
                                                                                                                                                                                                                                                                                                                                                                                      Molecular mechanism of retinoblastoma gene inactivation
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Homo sapiens (clone. RB [1,5]) toetas retina cDNA (c. mRHA
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Dryja, T.P. and Friend, S.
Human DNA in the diagnosis of retinoblastoma
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Fing.Y.K.T. T'Ang.A., Murphree,L.A. and Benedict,W.F. A method for detecting the predisposition to retinoblastoma and a method for detecting a retinoblastoma gene in tumors using a
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Database

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REFERENCE

TITLE AUTHORS

Young,P.E., Augustus,M., Carter,K.C., Ebber,K., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z. Cancer gene determination and therapeutic screening using signature

Mammalia: Eutheria: Primates: Catarrhini: Homonodae: Home

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SUMMARIES

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showing incomplete penetrance and mild expression of
                                                                                                                                                                                                                                                                                                                                                                                                             Structure and partial genomic sequence of the human retinoblastoma susceptibility gene Gene 80 (1), 119–128 (1989)
Gnadim, 2.,
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3253 CIGICIGACIACUACUTTGCCTTCTITIGAGCATALAGGICALGITEGCTCTIGITTTATE 3...4
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                                                                                                                                                                                                                                  Draft entry provided by
                                                                                                                                                                                                                                                                                                                                                                                              Li,F.P. and Weinberg,R.A. Deletions of a DNA sequence in retinublastumes and mesenchymal tumors: organization of the sequence and its encoded protein Proc. Null Acad. Sci. U.S.A. 84 (34), 9059-9063 (1987)
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Local Similarity 94.9%; Pred. No. 0;
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                                                                            1038 bp upstream of EcoRI site, chromosome 13q14.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia, Eutheria, Pri
1 (bases 243 to 4740)
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Homo sapiens (clone: RB-[1,5]) foctus retina cDNA to mRNA
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139. .2925
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/tissue_type-"retina"
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/db_xrof="taxon-9606"
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93.2%; Score 3148.4; DB 9; Length 4740;
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61
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Patent: US 5912236-A 1 15-JUN-1999;
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Broad spectrum tumor suppressor gener
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Db 1850 ITATITAANCAAAGAAAGAAAAAAAAAGATTCAACTGCAACAAGAACAACTGCAATCAA 17 A 19 A 1850 ITATITAAACAAACAAAAAAAAAAAAAAAAAAAAAAAAA	1970 TACAAAGTGATEGAAAGTTTTTATCAAAGCAGAAGCAACTTGACAAGAAAAAAAA	Oy 1294 TGCGCTCTTGAGGIIGTAAIGGCACAIAIAGCAGAAGAGAAG	OY 1174 GGAGTTCGCTPGTATTACCGAGTAATGGAAFCCATGCTTAAATCAGAAGAAGAAGAAGAAGAACGATTA 12xxx	Oy 1054 GIGAAIGCAAAAGAAGIAIACIGAAAAGAIGAAAGAIAIAGGAIACAACICIIIAAACAG III A III III III III III III III III	\$\text{\text{\gamma}} \text{\gamma} \text{\gamma} \text{\gamma} \text{\gamma} \text{\gamma} \text{\gamma} \text{\gamma} \text{\gamma} \qua	OY 874 GAGAGTERIANAGANAGANAGANAGANAGANGANAGANGANGANGANGA	2690 AAAATGTTIAITTOAAAAATTTTATAGCTETTATGAATICTCIIGGACHIGIAAGATCI	Oy 574 TOXCCTCGAACACCCAGGCGAGGCAAGAAGAGAGAGAGAGAGA

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I18496
                                                                                                                                                                                                                                                                                                                                                  Xu, H.-J., Hu, S.-X. and Benedict, W.F.
Broad-spectrum tumor suppressor genes, gene products and methods
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                                                                                               934 ATTCCTCCACACACTCCAGTIAGGACIGITAIGAACACIATCCAACAATIAAIGAIGAII 1633
                                                                                                                                                                                                                                                                                                         874 GACAGTTTTGAAACAGAGAGAGAACACGAAAAAGTAACCTTGATGAAGAGGTGAATGTA 544
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	2073 1311	AAGGATOTTOOTOATGAGTGTTOAGGAGAGACATTOAAAGG 	υγ 20 υb 13
	2013 1371	TATGGCATATGCAAAGTGAAJAATATAGACCTTAAATTCAAA 	фу 19 рь 14
	1953 1431	CASAATGAGTATGAACTCA IGAAAAAACAGACAT ETGGACCAAA ITA IGATGTGT FCCA 	ΩУ 18 Db 14
	1893 1491	CTTCTGTCTGAGCACCCAGAATTAGAACATATCATCTGGAGCCTTTTCCTTTTTCTTTTTTTT	оу 18 ръ 15
	1833 1551	CIGITITTATAAAAAAGIGITATICGCCTAGCCTATICTCCGGCTAAATACACTTTTGTGAAC	оу 17 16 16
	1773 1611	GAGACACAAGCAACCTCACCCTTCCAGACCCAGAAGCCATTGAAAT 	оу 17 Db 16
,	1713 1671	CCTGTAAGATCTCCAAAGAAAAAAGGTTCAACTACWGFGIAAATTCTACTGCA	уу 16 12 17
	1653 1731	GOFTGTOCLOTTAATOTTCCTCTCCAGAATAATCACACTGCAGCAGATY	оу 15 рь 17
	1593 1791	FTATTTGATCTTATTANACAATCAAAGGACCGAGAAGGACCAACTGATCACCTT	
	1533 1851	CATITAGAACGATGTGAACATCGAATCATGGAATCCCTTGCATGGCTC	
	1473 1911	TACAAAGTGATCGAAAGTTTTATCAAAGGAGAAGGGAACTTGACAAGAGAGAATGATAAA - - - - - - - - - - - - - - - - - -	
	1413 1971,	GGAACAGATTTGTCTTTTCCCAFGGATFCTGAATGTGCTTAATFTAAAAGCCTFFGATFT	
	1353 2031	TROROTOTTSACRETTSTAATRROCOCOCATATASCAGAAGTACATCTTCAGAATCTT - - - - - - - - - - - - - - - - - -	
	1293 2091	TCCATTCAAAATTTTAGCAAACTTCTGAATGACAACATTTTTCATATGTCTTTATGG LUHHIHHHHHHHHHHHH LUHHHHHHHHHHHHHHHHHHHH	
	– 10	GCAG LTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAACG - - - - - - - - - - - - - - - - - - -	оу 1174 рь 2210
	1173 2211	AAATTTGCTAAAGCTGTGGGA/AGGGTTGTGTGTGGAAATTGGATCACAGCGATACAAACT 	_
	11113 2271	GTGAATCCAAAAGAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTA 	
	1053 2331	HAAATTCAGCAAGTGAFCAACCFFCAGAAAATCTGAFTFCCFAFF	оу ч

Oy 2074 ANGARICINSTINATAMATICATIONACCOCCUENCY ANGARAS CHANANANANANANANANANANANANANANANANANANAN	_						•					,							
1131 TATGAPTETNITATICCIANTECTANTOCOCCUTENCISTO AGAGASTICAMANIA AS	ОУ	Dβ			Dp.	90 ()	ОУ	Qy Db	υb	ОУ	Å Š	Dp QA	Оу	Qy Db	Db y	0;	ДУ	Db Qy	ОУ
	154 AARTACTAATTTTACACATTAGATTTTATTTTACTATTGGAATCTGATATAGTGTGTC	094 ATTCACCAAAATTATCCIGAACICTTCIGCAAAATGGATATTATTAGAAATTAJAAAAA . 	034 ATGAACACCCTTAGAAAATGTGTCCTATCTATCTTCCAAATGCAATTTGATTGA	974 CAYATAGGYGAYGTFTGCYCTTGTFTTATTAATTIATATGTATATTITTTTAALLIAAC 	914 GCCCTAGAGTGGGAGTCCTGATAACCCAGGCCTGTCTGACTACTLICCTLCTTTTGTAG 	0854 TSTANSONSATISTITSSTETITSANASIAAAAISSUSISISIITAISSAIASIAA SAAIG 	794 TEAGTCATTGTEATTAIACAAGATTGAAAATCI IGTGTAAATCCIGCCAT LAAAAAGI 	34 TITGTGGATATAAAATGIGCAGATGCAATTGITTGGGTGATTCCTAAGCCACTTGAAATG 	674 ATGTGACTGTATAACTTT-SCAGGTTCTGTTTATGGCCACATTTAATATCTT-AGCTCTT 	614 TGAGGATCTCAGGACCTTGGTGGACACTGTGTACACCTCTGGATTGATT	554 ACACGAATGCAAAAGCAGAAAATGAATGATAGCATGGATACCTCAAACAAA	494 AAACATCTCCCAGGAGAGAGCCAAATTTCAGCAGAAACTGGCAGAAAATGACTCCAA 	434 CCTAAACCACTGAAAAAACTACGCTTTGATATTGAAGATCAGATGAGATGAAGCAGATGAAGT 	374 AATCAGATATGTAANAGNAGNAGTEGTTGAAAAGAAATTGTGTGAAGGAAGCAANCCT 	314 TCANGANTCTTAGTATCANTTGGTGAATCATTCGGGACTTCTGAGAAGTGCCAGAAAATA 	254 CTCAACAOTECATAT AAATTTEAGAAGGTEIGCSAAFASCAACAAAATGATTSTAAGA 	194 CETTACAASTITECTASTICAACCITACSGATICETAGAGGAACATCIATATITEACEC THEFITE HELLET	2134 IIG-AGIA16-CLICCA-CASCASCOCCIA/CIIGICA/CAAIACCICA/CAIIC TEVAASC 	1074 TATGAFTCTAFFATAGTAFTCTATAACTGGGTCTFGATGGAGAGAGCTGAAAAAAAAAA

Db 44 GRECANTO CETA POT TETATES WELVESTED STATEMENT STANDET AND STANDARD AND ANALYSIS AND STANDARD AND ANALYSIS AND STANDARD AND ANALYSIS ANALYSIS AND ANALYSIS ANALYSIS AND A	UY 182 CATTATUT GAGAAATTAAAGATA GAGAT GAGAGAGAGAGAGAGA	Db 134 GGGPCATGCCGCCAAAACCCCCCGAAAACCGCCGCCGCCGCCGCCGC	Ouery Match 73.8%; Score 2490.6; DB 6; Length 2994; Hest Local Similarity 93.7%; Prod. No. 0; Matches 2680: Conservative 0; Mismatches 4; Indels 177; Gaps 1; Oy 2 GGGTCATGCCGCCAAAAACCCCGCGGGGGGGGGCGCGGGGGGGG	AUTHORS Antelman, D., Gredory, R.J. and Wills, K.N. TITLE Retinoblastoma fusion polypeptides JOHRNAL Patent: US 6074850-A 4 14 JUN-2000; FLATURES Location/Qualitiers Source 1, 2994 /organism-"unknown" BASE COUNT 974 a 618 c 594 q 809 t		KESULT 12 AROURIBU AROURIBU 2994 bp DNA Libear PAI 14 FEB-2001	QY 3834 TETCTTCALCCAACTTATGITTIIAAATGAGATAIIGAIAGI 3377 	CY 3274 FACTATCATACTGACACACACACACACACACACACACACAC	UV 3214 TGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAAACCATATGA 3273 HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
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Autelman,D., Gregory,R.J. and Wills,K.N.
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2413 TCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAGCAGGCCCCCTACCT 2472
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retinoblastoma patients using single strand conformation
polymorphism analysis and polymerase chain reaction sequencing
Guadim, Z.,
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Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
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Hogg, A. and Cowell, J.K.
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                                                                            Draft entry and computer-readable copy of sequence for [1] kindly provided by S.H.Friend, 10-FEB-1988.
Location/Qualifiers
                                                                                                                                                                            Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors: organization of the sequence and its encoded protein term Null Arad Sci U.S.A. 84 (24), 9574-3663 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                             Human retinoblastoma associated (RB1) mkNA, complete M33647 J02994 M33647.1 GI:190945
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Enteleostemi; Mammalia, Enteria, Frimates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    retinoblastoma protein.
Humo sapiens (clone: p4.7k) cDNA to mRNA.
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                                                                                                                                                                                                                                                 Li, F.P. and Weinberg, R.A.
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                                                                                                                                                                                                                                                                  Friend, S.H., Horowitz, J.M., Gerber, M.R., Wang, X.F., Bogenmann, E.
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/db_xre1="taxon:9606'
/map="13q14.2"
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                                                                                                                                                                                                                                                                                           481 GCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCCAGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 CTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAAGAAATTGAT 330
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TOGATATO FACTGAAATAAATTO TOGATTOO FOOTAAAAAGTI FOTTTOO ATCACATTI FITA 600
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RVL.IKEEEYDSIIVFYNSVEMORLKINIIQYASTREFTLSPIPHIPRSPYKEPSSPLR
IPRGNIYISPLKSPYKISERILPIPEKMIPRSRILVSIGESEGTSEKFOKINOMVCNSD
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SPLEDLIKQSKDÆFGPTDHLESAGPLNI PLQNNETAADMYLSPVESPKKKGSTTRVNS
TANAETQATSAFQTQKFIKSTS I SLEVKVYÆLAVLÆLNTLGERLLSEHPELEHTIMT
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MICVLDYFIKISPPMILKFPYKTAVIPINGSPTTPERGONRSARIAKOLENDTRIIEV
LOKEIIBONIDEVKNYYFKNFIPFMNSLOLVTSNGLPEVENLSKRYEEIYLKNKDLDAR
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/translation-"MPPKTPRKTAATAAAAAAARPPAPPPPPPPEEDPEQDSGEEDLPL
/translation-"MPPKTPRKTAATAAAAAAAARPPAPPPPPPPEEDPEQDSGEEDLPL
VRLEFFETTEEDPFTALCQKLKTPDHVRFRAWILWFKVSSVUGVLGGYTQKKKELWGTC
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l___4600
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23	- Y	1291 ATGCTTAAATCAGAAGAAGAACGALTATCCALLCAAAATTILTAGCAAACTTCTGAATGAC 1350	•
23	Db	1231 GAAATIGGAAT AY AG GALAY AAAY ILGGAG ICGYTIGIALIAG GAGTAATGGAATCC 1290 	
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22	Qγ	1/1 AAGGATATAGGATACATCTTTAAAGAGAAAATTTGCTAAAGCTGTGGGGACAGGGTTGTGTC 1	
22 -	136	1111 CICATITECTATITTAACAACIOCACAGIGAAFCCAAAAGAAGTAFACTGAAAAGAGTG 1170 	
22	Db Db	1051 AACACTATECCAACAATTAATSATGATTTTAAATTCAGCAAGTGATCAACCTTCAGAAAAT 1110 	
21	. Db	991 AGTANCCTEGATGANGAGGTSANTGTANTTCTCCACACACTCCAGTTAGGACTGTTATG 1050 	
N 2 1	. Db	931 GATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGAACACCACGAAAA 990 11111111111111111111111111111111111	
20	Ov Ov	871 CGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCAT 930 	
. e .	ov Pb	811 ATGAATTETETTUGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTTTTCTAAA 870 	
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	O DB 4	451 TOMATATOTACIGAAATAAATTOTGOATTGGTGCTAAAAGTTTCTTGGATCACATTTTTA 510 	-
	0 Db 5	391 GYACTECTECAGCAAATTGJAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGT 450 	
14	0	431 AVYAGTAVYAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAAGTATGATGTATTGTTT 390 	-
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                                                                                                                                       3478 CAGAATGTAAAAGAACTTACTGATTATTTTCTTCATCCAACTTATGTTTTTAAATGAGGA 3537
                                                                                                                                                                                                           3391 CAGAATGTAAAAGAACTTACTGATTATTF1CFTCATCCAACTTATGTTTTTAAATGAGGA 3450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3031 GICHACTACTATOCCTTCTTT NACCATATAGGIGATGTTTGCTCTTGTTTTTATTAA 3090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTGACTACTTTGCCTTCTTTTGTAGCATATAGGTGATGTTTGCTCTTGTTTTTATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGOCCACATITAATATATTCAACATTITITATTATATAAAAATGTCAGATGCAGATGCAAATTTT 2937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSGACTTCTGAGAAAGTTCCAGAAAATAAATGAGATGGTATGTAAACAGGACGACGACGGTGTGCTC
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AUTHORS
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Matches 3452;
                            Best Local Similarity
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
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87149066
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA69807.1"
/db_xref="G1:190959"
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139. .2925
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/tissuc_type-"retina"
/dev_stage-"foetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene-"RB1"
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/db_xrei-"taxon:9606"
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                            97.1%;
                                                            96.0%; Score 3322.8;
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                                Pred. No. 0;
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Length 4740:

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1 (bases 243 to 4740)
Lee.W.H., Bookstein, R., Hong, F., Young, L.U., Shew, C.Y. and Lee, E.?
Buman retinoblastoma susceptibility gene: cloning, identification.
1038 bp spairmam of EcoPI site; chromosome 13q14.inq14.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 85 (16), 6017-6021 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular mechanism of retinoblastoma gene inactivation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Difeleostomo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (clone: RB-[1,5]) foetus retina cDNA to mkNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human retinoblastoma susceptibility mkNA, complete cas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ., Bookstein,R., Young,L.J., Lin,C.J., Rosenfeld,M.S.
                                                                                                                                                                                                                                                                                                            LFLDHDKTLQTDSIDSTETQRTFFKSHLDEEVHLIFFHTTVKTVMHTIQOLMHILSSA
                                                                     RVI.KKSAKGSNYPKYI.KKLEPTOLEGSOLATOSEHLITGESEE QUELAEMYS EEFIMGK.
KMNDSMDTSNKEEK"
                                                                                                                                       RVLIKEEEYDSIIVFYNSVFMQRLKINILQYASTRPPTLSFIPHIPRSPYKIYSSPLK
IPOGNIYISPLKSPYKISEGLFTFTKMTFESEILVSIGESTCISEKT EITH WYSTSSPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MECVEDYFIKESFPMLEKEPY KEAVEL I NOSEREPEVENESK KYELEVEKKELLEKKELLEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANAETOATSAFOTOKPLKSTSISISTYKKVYRLAYLRINITICEKILISEHPITTELETEK
LEGHTLQNEYELMEGEHLIGIMKTSKYZITEVENIILEEELITYTAVELETHAVLETEK
                                                                                                                                                                                                                                                                                   SPLEDLIKQSKDREGPTDHLESAGPLALPLQNNHTAADMYLSEVESEKKKSELIKVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"retinoblastoma susceptibility protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gopy of sequence in [1] kindly
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223 CATITION	Dh		=
2008 CATTIGG	Qy	CATGATAAAACTCTTCAGACTGATTCTATAGACACTTTTTGAAACACAGAGACACCACCAC	٩
2173 ATCATCTO	qq	BBB AAAN GATAN GAAGAAATTA ICTTAAAAATAAAGATCI AGATA ICGAATA ITIA TETTI IGGAY 927 TITTI TITTI br>093 AAAN GATAN GAAGAAATTI TA ICTTAAAAATAAAGA ICGAGA ICGAAGANIYATI TITTI IGGAY TITSI	1093
1948 ATCATCIO	Vγ	TITALGAALIS TCITGGAACI IGIAAK.AICI AA IGGAACI ICIAGAGGI TGAAAAA ICITICI	
2113 TATCTCC		TETATICA ATTEVIO TETATA TA ATTEVIO PARA LA PARA PER LA ALIGUACITE CAGAGGITGAAAAR ETTTCT	<u> </u>
1888 TATCTCC	γo	PROPERTY OF COMPLETE AND A COMPLETE AND AND AND A COMPLETE AND	: :
υ s	Db	748 AAAVAAGTGAATGTAATATAGATGAGGTGAAAAATGTTIAITTGAAAAATTTTATAGCCT 807	4.7
1828 CAGAAGG	Ç Ş	913 AGRAGITOPACGPATAGPAAAACAACTAGAAAATGATAGAAGAATTATTGAAGTTCTCTGT 972	- Y
1768 ACTACGC	Ç 4	688 AGGAGTGGAGGGATAGGAAAAGAAAGTAGGAAAATGATGA	5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4580)
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Pytent: NS 5912235-A 1 15-JUN-1999;
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297. COATAAATTOTTIAACITACIAAAAGAAATIGATACCAGTACCAAACI GATAATATTAT 357
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                                    TIGTAGEAGATTGTTTCCTCTAAAGTAAAATGCTGTGCTTAAGGATAGTAAGAAT 4/2
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                                                         1 (bases | to 3242)
xu,H-71, Hu,S-7X, and Henedict,W.F.
Broad spectrum tumor suppressor genes, gene products and methods
for tumor suppressor gene therapy
Patent: US 5496731-A 1 05-MAR-1996;
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AATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGAT
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96 72	2037 OTATOGOATATOGAAAGTGAAGAATATAGAGGTTAAATTGAAAATGATTGTAAAGAGGATA 209 1711-1711-1711-1711-1711-1711-1711-171	99 72
36	1977 GCAGAARGAACRARGAACROARGAGAGAGAGAGACAAACRAGAGAATTATGALGTGREGCAR 203 	Qy Db
76 92	1917 COTTOTGTOTGAGGACCCAGAATTAGAACATATCATCTAGACCCTITTCCAGGACACACCCT 197	Db Qy
16 52	ACTGTTTTATAAAAAAGTGTATCSGCFAGCCFATCTCCGGCFAAATACACTTTGTGAACG 1 	υψ
56 12	ACAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTC 1 	dd VV
96 72	TOUTGTAAGATCTOCAANGAAAAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGC I	90
36 32	TROTTOTOTOTOTIAATOTTOOTO, COAGAATAATOACACHGCAGGAGGAGATATGTATGTTTO T	96 50
76 92	TITATTIGATORIARRAACAAROAAROAAGGAGGAGGAGGAGGAACHGARGAGGAGGAGGATAACHGARGAGGAGGAGGAGGAGGAGGAGGAGGAGGAAGGAACHGARGAGGAGGAAGAAGGAACTGARGAGGAGAAGGAAGGAAGGAAGAAGGAAGAAGGAAGAA	qq V
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AGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGGCAGAAAAGGAAATGAATA	TTGAAGGATGAGATGAAGCAGATGGAAGTAACATCTCCCAGGAGAGTCAGAATTTCAGC	AAAGAAGI GCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACCCTTTT 	STTOCASAAAA IAAA ICAGA FIGI A IGI AACA 	TGCCAACAACAACAAAATGACTCCAAGATCAAGAACCTTAGTATCAATACTAATAATAT 	TYPCCTGGAGGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTTGAGAAGGTCCATATAAAATTTCAGAAGGTCCTGAAGAGTCCATATAAAATTTCAGAAGGTCCTGAAGAAGTCCATATAAAATTTCAGAAGAGTC	TGTCACCAATANCEICACATHCCICGAAGCCCTTACAAGITECCTAGTTCACCCTTACGGA	TCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCTACCT	TCAAACCTGTTTTGATCAAAGAAGAGGGGGTATGATTGTATTATAGTATTCTATAAACTGG 	TTANATTE ANANTENTISTANENENENENENENENENENENENENENENENENENENE	ATTIGGACCAAATTATGATGTGTTCCATGTATGCCATATGCAAAGTGAACAATATAGACC	TCATICTIGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAGAC	ATCTCCGGCTAAATACACTTTGTGAACGCCLLCTGTCTGAGCACCCGAGAATTAGAACATA 	AGAAGCATTGAAATCTACCTCTCTCACTGTTTATAAAAAAGTGTATCGGCTAGCCT 	CTACGCGTGTAAATTCTACTGSAAATGCAGAGACACAAGCAACCTCAGCCTTCAGACACCCTTAGACACCCCTAGACCTCAGACCTCAGACCTCAGACCCCCAGACCACACACCAC	ATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAAGGTTCAA 	GAGAAGGACCAACTGATCACCTTGAATCTGCTCTCTCTAATCTTCTTCTACAATA	AATCCCTTGCATGCCTCTCAGATTCACCTTTATTTGATCTTATTAAACAATCAAACAATCAAACAACCAATCAAACAATCAAATCAAACTTATTTGATCTTATTTGATCTTATTAAACAATCAAACAATCAAAAACAATCAAAAACAATCAAAAACAATCAAAAACAATCAAAAACAATCAAAAACAAATCAAAAACAATCAAAAACAATCAAAAACAATCAAAAACAAAAAA	GTGAACATEGAATCATGG - - - - - - - - - - - - - - - - - -
2668	F F B Z	2548 2773	2488 2713	2428 2653	2368	23.43	2248 2473	2188 2413	2128 2353	5.67.7 5.068	2008	1948 2173	+117 8881	1828 8781	1768	1708 1934	16.4 B 1873	1813

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434 GGCCAATOTICTIATIOTENTACEACOACTITICACCTIACATGAGATGAGATGTCCTTTCACTTTTTACTC
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OS Unidentified
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PN JP 2001503638 A/2
PD 21-MAR-2001
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PR 15-NOV-1996 HS 08/755517,14-FFH-1997 HS 08/
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Antelman,D., Gregory,R.J. and Wills,K.N.
Tissue specific expression of retinoblastoma protein
Fatest: Jr 2001=83838 A 2 21-MAS 2001
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    Mismatches

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                      1514 CCATGCTTAAATCAGAAGAAGAAGATTATCCATTCAAAATTTTAGCAAACLLCLGAALT
                                                                     1289 CCATGCTTAAATCAGAAGAAGAACGATTATCCAITCAAAATTITAGCAAACITCTGAAT; 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734 TATTAGGTAAAGGGGAAGTATTAGAAATGGAAGATGA (CTGGTGATTTGATT ! ^AST LAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | A] GA I AAAAC ECI I CACAC I GAATTO TATACACACACI I I I GAAACAC AGAGAACAC CAGGAA | 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGAAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTG 145×
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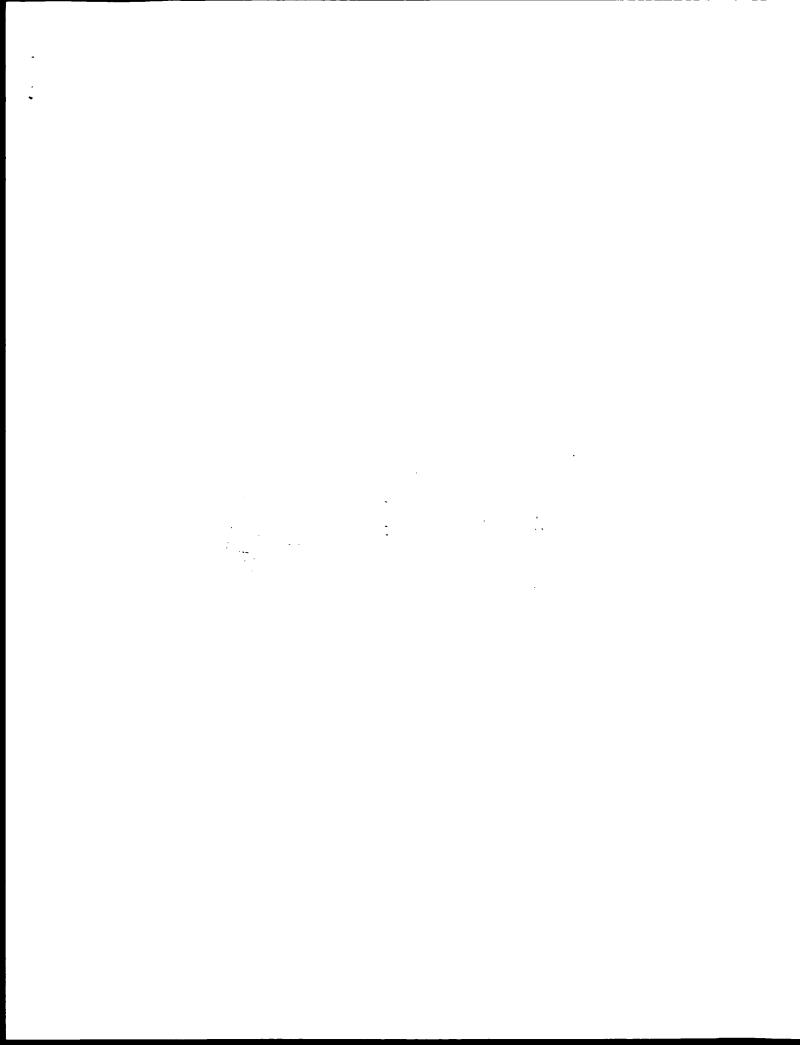
	2429 TECHTOACTICTUAGAAATTICCAGAAAATAAATCAGATEGTATETAACAGEGACEGTGTGC	9
2653	2594 TGCCANCACCANCANANATGACTCCANGATCANGAATCTTAGTATCAATTGGTGAATCAT	Ē 5
	2534 TECCHOGAGGGAAGATCTATA FITCAGGCCCTGAAGAGTCCATATAAAATTCAGAAGGTC	Ē
2533 2368	2474 TGTCACCAATACCTCACATTCCTCGAAGGCCTTACAAGTTTCCTAGTTCACCCCTTACGGA 2309 TTCCTGGGGAGGGAACATCTATATTTCACCCCCTGAAGAGTCCATATAAAATTTCAGAAGGGTC	<u> </u>
2308	2249 IGICACTAATACCTCACALITCCTCGAAGCCCTTAGAAGTTTCCTAGTTCACCCCTTACGGA	70
2248 2473	2189 TOTTOATOCASACACTSAAAACAATATTTTGCAGTATOCTTOCACCAGGCCCCCTAGGT 1HHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	15 VQ
2188 2413	2129 TEAAANSETSTTTGATEAAKSAAKSAAKSAGKETATGATTGATTATAKSTATTCTATAAKTEGG HIILIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	å Š
2128 2353	2069 TEAAAEECAAAAFCATECTAACAACAACAACAACGAECTECTCATGCTGTTCAGGAGACAT 	gg Vy
2068 2293	2009 ATTTGGACCAAATTATGATGTTCCATCTATCKCATATGCAAACTGAAAAAATATAGACC 	PF Qy
2008 2233	1949 TOATOTGGACCOTTTTCCAGCACACCCTGCAGAATGAGTATGAACTCATGAGAGACAAGGC HHHHHHHHHHHHHHHHHHHHHHHHHHH	DE CY
1948 2173	1889 ANCHORODIAAATACACHTHGIGAAACGCCTHCHGIGTGTGAGCACGCGGAGAATHAGAACATA 	₽ 9
1888 2113	1829 AGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGGCT 	P Cy
1828 2053	1769 CTACGCGTGTAAATTCTACTGCAAATGCAGAGACACAAGCACGCGTCAGGCTTCGAGAGGC HILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	de V
1768 1993	1709 ATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAGGTTCAA 	44
1708 1933	1649 GAGAAGACYAACTGATCACCTTGAATCTGCTTGCTCTTAATCTTGCTCTCCAGAATA 	å Å
1648 1873	1589 AATOOOTTGOATGAOCTCTOAGATTOAVCTTTATTGATCTTATTAAACAATCAAAGGAGC HHILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	υ ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο
1588 1813	1529 AAGG AAC FIGACAAGAGAAA IGA LAAAACA FEFAGAACGATGTGAAGATCGAA FCATGG HELLIH HILLIH H	5 A
1528 1753	1469 ATGTGGTTAATTTAAAAGGCTITGATTTTTAGAAAGTGATGGAAAGTTTTATGAAAGGAG 	å Å
1468 1693	1409 GYAGAAGTACATCTCAGAATCTTGATTCTGAAACAGATTTGTGTTTTCCCATGGATTCTGA 	<u>\$</u> &
1408 1633	1349 APAACATETETCATATGTCTFTATTGGCGTGCGCTCTTGAGGTTGTAATGGCCACATATA 140 	40

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                           434 GGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTTTACTG 493
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                                                                                                                                                         374 AGAAAGTTICATCTGTGGATGGAGTATIGGGAGGTTATATTCAAAAGAAAAAAGAAACTGT 433
                                                                                                                                            / Match 76.9%; Score 2661.8; DB 6; Length 2994; Local Similarity 96.7%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                              Shepard, H.Michael. and Wen, S.Fen.
Characterization of a novel anti-pll0.sup.RB monoclonal antibody
Patent: US 5710255-A 2 20-JAN-1998;
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Sequence 2 from patent US 5710255.
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	748 973	189 GGAGTGCACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTA {	ру 6
	688 913	29 ATAAAACAGCTGTTATAGCCATTAATGGTTCAGCTGGAACACCCAGGCGAGGTCAGAACA 	11p 8
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<u> </u>	568 793	09 TATTAGCTANAGGGGGAAAGTATO	уу 5 19b 7
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	448 673	RRU HOCACTO FOAGCAAATTOGAAGGACACGTGAACTTATATATTTGACACACACCCACCA 	Db 6
	388 613	129 ATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAAGTATGATGTATTGT 	рь 3 5
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2488	429 TOGGGACTTOTGAGAAGTTOCAGAAATAAATGAGATGGTATGTAACAGCGACGTGTGC 	Ωу		
1. A.	2369 TGCCAACAACAACAAAAHGACTCCAAGATCAAGAACCTTAGTATCAATTGGTGAATCAT 	Qy Db		
54.8	2309 TTCCTGGAGGSAACAICTATATTTCACCCCIGAAGAGGCCATATATAAATTTCAGAAGGTC 	Оу	-	
24.78 2533	2249 ISICACYANIACCICACNITCCICSANGCCCIIACAAGIIICCCIAGIICACCCIIIACGGA [4d 7d		
224 d 2473	2189 TCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAGCAGGGCCCCTACCT 	Oy Db		
21 H H	2129 TOAAACGTGTTTTGATCAAAGAAGAGGAGTATGATTCTATATAGTATTCTATAACTCGG 	QY Db		
511.4 87.17	2069 TTARATTCARAATCATIGIANCAGCAINCANGGATUTICUTUATGCTGTTCAGGAGACAT .	da Võ		
57.43 8402	2009 ATTTGGACCAAAFTATGATGTTGCATGTATGGCATATGGAAAGTGAAGAA I A FAGACC 	Qy Dh		
2008	1949 TOATCTSGACCCTITTECCAGCACACCCTSCAGACISAGIATSAACECATSAGACACGC 	ûy Db		
194 217	1889 ATCTCCGGCTAAATACACTTTGTGAACGCCLICIGICIGAGCACCCAGAAIIAGAACATA 	фу Оγ		
F: 00°	1829 AGAAGCCA PIGAAA ICLACCIC LCITICACIGITITA IAAAAAAGIGIA ICGG TAGCCI HITHHIHHHIHHHIHHHIHHHIHHHIHHHIHHIHHIHHHIHHHIHHIHI	Оу		
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1768	1709 ATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAASSTTCAA 	QY Db		
1764	1649 GAGAAGGACCAACTGATCACCTTGAATCTGCTCTGTCCCCTCTCCAGAATA 	Qy Db		
164×	1589 AATGCCTIGCAIGGCICICAGAITCACCTTTATTTGATCTATTĀAACAATCAAAGAGGCCC 	ψy Đì		
181.	1529 AAGGCAACITTSACAAGAGAAATGATAAAAACATTTAGAACGATGTGAACACCGAATCATGG 	dd VŸ		
152 175	1469 AIGTGCTTAATTTAAAAGCCTTTGATTTTTACAAAGTGATCGAAAGTTTTATCAAAGCAG 	Qу		
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Search completed: January 17, 2003, 18:08:53 Job time: 5779.07 sees



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Retinoblasiona fusion polypeptides
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Antelman, D., Gregory
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190	(:1yProThrAspHisLeu(:)uSerA1aCysProLeuAsnLeuProLeu(:)nAsnAsnHis 	Ç
549 1878	LeuAlaTrpLouSerAspSerProLeuFbeAspLeuIleLysGlnSerLysAspArgGlu 	da Vy
529 1818	ASBLEGSFBYARGCIUMCT (10) ySHiS) 00G BALGCYSGLUHESAFGLLEMELGIUSUF 	dq Vy
509 1758	LeuAsnLeuLysAlaPheAspPheTyrLysVallleGluSerPhcIicLysAlaGluGly 	g çç
489 1698	SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIleLeuAsnVal	96.
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4 0	LeuLysSerGluGluGluArqLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 	ρb
	TloslySerSlbArgTyrLysLeuGlyValArgLeuTyrTyrArgValMotGluSerMot 	<u> </u>
	AS\$ eClyTyT ePhelySClutySPheAlatysAlava;ClyC)nClyCySValGlu 	qd A5
<u>~</u> ~	heAsnAsnCysThrValAsnProLysGluSerIleLeuLysArgValLys 	ФУ
369 1338	ThrileGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGluAsr 	qq çy
349 1278	ASTÜRVASPĞÜ GĞÜ AVALASTIVA İLLEPT OPTOHISTTAT POVALAT ÇITAYVA 	Фb
329 1218	LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArqThrProArqLysS 	da YY
309 1158	TyrfiluflifleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHi 	40
289 1098	ASESC TARROLY SARVATTE FOR ASESC TY CONTROCTOVATOL ASESC ASESC TARROLY SARVATOR ASESC ASES	ОУ
269 1038	#HSGH:CysAspHleAspGluValLysAspValTyrPhcLysAsnPheIleProFhcMct	da VV
249 978	AlacralleAlaLysclnLe-cclaAsnAspThrAcralleTlecluvalLe-ccystysclu 	£ 6
F. 1.3	ThrAlaVallicProficAsmClySerProArgThrProArgArgClyCinAsmargSer 	Db Cy
858	HITTHITTIATAAACTCTCACCTCCCATGTTGCTCAAAGAACCATATAAA	đq

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RESUL AR207 Locus	Db	Qy	Db	0v	οξο	Qy	40	Qy	Db	VQ	Db	Qy	d:i	Qy:	Ωb	Qy	Db	Qу	qu	Qy:	dci	Qy	Db	NO V	D 49) [YQ Y	타	Оy	Ðψ	Qy	qq	Ş.	Dþ
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AR207831	CATACCTCAAACAACGAAGAG	spThrSerAsnLysGluGl	CTGGCAGAAAIGAC FTC FACT	uAlaGluMetThrSerTh	GGATCAGATGAAGCAGATGGA	recraspGlualaaspGl	AGAAGTGCTGAAGGAAGCAAC	rqSerAlaGluGlySerAs	ACTIOTICAGAAGTTOCAGAAA	rSerGluLysPheGlnLy	ACACCAACAAAAATGACTCCAAG	rProThrLysMetT	GGAGGGAACATCTATATTTCA	lyGlyAsnIleTyrIleSe	CCAATACCTCACATTCCTCGA	rolleProHislleProArg	ATGCAGAGACTGAAAACAAAI	lnArgi.eul.ysTl	CGEGETTTEGATICAAAGAAGAGAGA	rgValLeuIleLysG	TTCAAAATCATTGTAACAGCA	ysileflevalThrAl	AACCAAATTATGATGTGTTCC	In I Jewet Met des Sei	TOGACCCUTTUTCCACCACACACOC 	GGCTAAATACACTTIGIGA	ArgleuAsnThrleuCysGlu	TGAAATCTACCTCTCT	ProbedlysSerThrSetLeu	TAAATTOTAATAAAA	gValλsnSerThrAlaλs	ACTROCAGCAGATATGTATGTT	rAlaAlaAspMctT;rLe	GGACCAACIGATCACCITGAA
2994 bp	- 8	Lys 897	TEGAACACGAATGCAA	raThrAraMet(AGTAAACATCTC:	SerlysHislea	TECTICCTAAACCAC FGA	ProProLysProLe	ATAAATCAGATGGT	IleAsnClnMetVa	AGAICAAGAAICTIAG	gSerArgile	CACCCC IGAAGAGTCCA	Ser!	AGCCCTTACAAGTTTCC	SerProTyrLys	AFATT TTGCAGIAIGCI	leLeuGlnTyrAla	ACTATIGATTOTALII	luTyrAspSerIl	HITTITION TO THE PROPERTY OF T	TyrkysAspkeuPr	ATSTATSSCATATSS	Mot march all posse	LEUGIDASDGIUIY 		uArgLeuLeuSerGlu	TCACTGTTTT.	SerTæuPheT	ACACACACAA	GluThrGlnAl	TCTCCTCTAAGATC	SerProValArgSo	ATCIGCTIGICCICII
VNG			AAGCAGAA	sGIn!	**************************************	70.0	AAAAAC	ysLysL	ATGTAACAC	ysAsı	Z	a)Ser	CATATAAAA	rL,s	TAGT	oser:	(TOCACCAG)	SerThi	ATAGIT	eVa.	TCAIGCIGT	SA la	ANAGTGANGAN	į	VLCAVCICV VLCAVCICV VLCAVCICV	ACCCA	Hispro		711.751.75Vaii	A -	- H - H - S	CTCCAAAGA	~:	MICTICO
linear			AATGAATGA	SMOTASTIA:	COMMITTEN	LysPheC	TACGCTITTA	uArqPheAs	CAGCGACCGIGI	sp A r qVa	HIGGIGAAL'A	ed) yd 1 i	ATTTCAGAAGG	erGludi	ICACCCTTAGG	SLOUAT	HILLITTE	roProIt	APPETAFAACTO	7rAs:	TCAGGAG	lGlnGl	TATAGA	reach loac		AATTAGAACA	Chul.euGluHi	ATCGGCTAGC	yrArqi.cuAlai		aPheG1	AAAAAGGIIC	si.ysciy	стстссабал
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Oy 190 CysValledasplyrPhellelysLedSerProProMetLedLedLysClaProTyrLys 209	OV 170 AldrysslychuvallaeudinmetchuaspasplaeuvallieSerphedinlaeumetheu 189 	OV 150 ILeSerThrGluI[eAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 169 	OY 140 LeuPheSerLysLeuGluArdThreYsGluLeuT]eTyrLeuThrGInProSerSerSer 149 DD 619 CTCTTCAGCAAATTGGAAAGGACAIGIGAACTTALALATTTGACACAACCCAGCAGTTCG 678	OY 110 SerThrLysValAspAsnalaMetSerArgteuteutgstysTyrAspValLeuPheAla 129	Oy 90 GlüfysAsülleGlüfleSerValffisLysPhePheAsüLeüLeüLysGlüfleAspThr 109 	OY 77 VALASPLEUASPGTUMETSOEPHETHTPHETHTFHEU 89 DE 439 ATCTGTAICTTIAFTGCAGGAGTTGACCTAGATGAGATGTCGCTTCACTTTTACTGAGCTA 498	Db 479 GTTTCATCTGTGGATGGATGGAGTTTATATTCAAAAAAAA	Oy 61 CysGlnLysLvdLysIleProAspHisValArqGluArqAlaTrpLeu	OY 41 ASplandrolandvalArglanddupheGludlufhrGludlufroAspPheThrAlalan 60 (11111111111111111111111111111111111	OY 21 ProAldProProProProProProProProBluGluAspProGluGluAspSerGlyPProGlu 40	ysThrProArqLysThrAld - - - - - - - - - - - - - - - - - -	99.45% Indels: 6 Gaps: 697) x AR207831 (1 2994)	Pred. No.: 0 Longth: 2994 Score: 4605.50 Matches: 897 Percent Similarity: 96.66% Conservative: 0 Rest Local Similarity: 96.66% Mismatches: 0	PASE FOUNT 974 d 618 c 593 d 809 t ORIGIN Allemment Scores:	2	Unclassified. 1 (bases 1 to 2994) Antelman.D., Gregory.R.J. and Retinoblastoma fusion proteins	SOURCE Unknown. ORGANISM Unknown.	DEFINITION Sequence 3 from patent HS 6379927. ACCESSION AR207831 G1:21507687
рр 1873 с	1819	1759	1699	1639	450 1579	1519	1459	390 1399	1339	350 1279	330 1219	OY 310 L	Oy 290 : Dh 1099 I	Qy 270 A Db 1039 A	27 200 H		859	Db 799 T Qy 210 T
GTyProThtAspHtsLendTuSerAladysProLenAsuLenProLendTuAsnAsuHis {		ASILEHITIA (GALIMET LIELYSH SLEGISTAACGYSTIHLISAFQ LEMETGIUSer I HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	LEHASILEHLI YSA I BELOARPHARYELYS VALLI LOGIA GAPERALIS I IYA IJARI RELY LEHHELHILLI LIHHELHILLI HILLI HILLI HILLI HILLI HILLI HILLI HILLI HILLI CHILLI CITAALTI AAAAG CAGAAGA CAGAAGA C	SETIONS FOR INASTLEMANDS OF BY A PROPERTY OF A CHARACTUAL HILL HILL HILL HILL HILL HILL HILL HI	LEPREHISMETSELLERUKIAGYSKIALERGIAVALVALMATATIKTYSEAKA HIHHHIHHHHHHHHHHHHHHHHHHHHHHHHHAA ATTITICATATGICTITATIGGCGTGCGCTCTTGAGGTTGTAATGGCCARATATAGCAGA	LeulysSerGluGluGluArdLeuserTleGluAsnPheSerLysLeuleuAsnAsyAsn 	THE CLYSTED THAT THE TEST CLYSTE OF CHISTORY OF A PART AND CATEGORICAL THE THE THE THE THE THE THE THE THE THE	ACPTIEGIYTYY IIOPKEUYSGIHUYSPHOALALYSALAVAIGIYYDIBGIYOYSVAIGH 	LESSETYPPH-ASSIASBICYSTB: Vallaspeolysigluser i Leta-olysiagval ilys- LITH LITH LITH LITH LITH LITH LITH LITH	The High and an amore world in epidens geral a Son as politizar of orthogonal and an analysis of the control of the High High High High High High High High	ASDLEUASPGLUGLUVALASDVALLIEPTOPTOHISTDEPTOVATAEGTDEVALM-CASD 	LysThrLeuGln1hrAspSer11eAspSerPhedJuThrGlnAraThrFroAratlysSed 	Tyrdisdistetyrionlysasniysaspiouaspalaarqioudsotouaspalisasp 	AsnSerLeaGlyLeaValThrSerAcnSlyLeaFroSlaValSlaXsnLeaSerLysArq 	HISSERS, ASSERT MAY PRESENTED ASSEVED THE FOR SEASON PROMOTE THE FOREST SEASON PROMOTE THE FORES	A LIA E GHEALL A I SGIDLE (GIUA STA SPILT A E GHEALL (GIUA TE GET SE STA) SGID THE HELLE H		TGIGICCITGACIATITIATTAAACICICACCICCCATGITGCICAAAGAACAACAIAIAAA ThrAlaVallleProlleAsmGlySerProArqThrProArqArqGlyGlaAsmArqSer

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HD009728
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            DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgSerAlaGluGlySerAsaFroProLysFroLeuLysLysLeuArgPheAspIleGlu 849
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        Tissue specific expression of retinoblastoma protein
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2779 GGATCAGATGAAGCAGATGGAAGTAAACATCTGCCAGGAGAGTCCAAATTTCAGCAGAAA 2838
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Mammalia; Entheria: Primates; Catarrhini; Hominidae; Homo.
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RVI, KYANAGISKUPK QUKULEH INGSTULADISEHIJIPIESKE QUKI AHMISTET KMOKO
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Proc. Natl. Acad. Sci. U.S.A. 89 (13), 6177-6181 (1992)
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                                                                                                            Mutation data provided by Dr. B.L.Gallie
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Recombinant adenoviral vector and methods of use
Patent: US 6210949 A 7 03-APD 2001;
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Draft entry and computer-readable copy of sequence in \{1\} kindly provided by P.Bockstein, 2^{n}-Arm 1987.
                                                                                                                                                                                                                                                                                                                                                                                  retinoblastoma susceptiblity. Here safies (close, RB-(1,5)) feetus retina cDNA to mkNA Homo sapiens
                                                        Proc. Natl. Adad. Sci. U.S.A. 85 (16), 6017-6021
88320373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human retinoblastoma susceptibility mRNA, complete cds M154\,00
                                                                                                                     Molecular mechanism of retinoblastoma gene inactivation
                                                                                                                                                             Lee, E.Y., Bookstein, R., Young, L.J., Lin, C.J., Rosenfeld, M.G.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo-
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                                                                  429 %LeuLysSerGlaGlaGlaArqLeuSerTleGlaAsuPheGerLysLeuLeuAsnAspAs 449
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                                                AACACCAACAAAAATGACTICCAAGATCAAGATCTTAGTATCAATTIGGTGAATCATTICGG 2657
                                                                       OThrProThrLysMetThrProArgSerArgileLeuValSerTleGlyGluSerPheG1 809
                                                                                                                                           TGGAGGAACATCTATATTTCACCCCTGAAGAGTCCATATAAAATTTCAGAAGGTCTGCC
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                                                                                                                                                                                                                                         CMctGlaArgLcuIySThrAsalleLeuGhtYrAlaSetThrAtgPtoFtoThrLcuSe 749
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCITETTTEGATEAAGAAGAAGAAGTATGAITCTAITATAGTATTCTATAACTCGGTCTT 2417
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sargValleufletysCluGluGluTyraspSeriletleValPheTyraspSerValph 729
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Sequence 1 from Patent WO 8906703.
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Dryja, T.P., Erlend.S. and Yand-11,D.W.
DIAGNOSIS OF RETINOBLASTOMA
Patent: WO 8906703-A 1 27-TH. 1989;
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† :	IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThiTyrS+FArg -	450	Qy
-	CTTAAATCAGAAGAAGAACGATTATCCATTCAAAAATTTTAGCAAACTTCTGAATGATAAC	1 381	d(I
444	LeuLysSerGluGluGluArqLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn	430	Сy
ŝ	ATTEGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACCGAGTAATGGAATCCATS	1321	Дb
4.19	leClySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArgValMettluSerMet	410	Qy
409	390 AspileGlyTyrrlePheLysGluLysFheAlaLysAlaValGlyGlnGlyGysValdlu 409 	390 1261	Дy
1250	ATTTCCTATTTTAACAACTGCACAGTGAATCCAAAAGAAAG	1201	dd
4	IleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIleLeuLysAraValLys		Qy
	ACTATCCAACAATTAATGATGATTTAAATTCAGCAAGTGAACCTTCAGAAAAAGT	1141	Db
*	ThrileGinGinLeuMetMetHeLeuasnSerAlaSerAspGinProSerG.::asnLeu		ОУ
1.4	AACCTTGATGAAGAGGTGAATGTAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC	1081	Db
£	AsnLeuAspGluGluValAsnVallleProProHisThrProValAryThrValMetAsn	330	Cy
ī	######################################	1021	del
î.	LysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArqThrProArqLysSer	310	Qy
1 - 2 - 2	TACGANGAAATTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATCATGAT	961	pb
:: -4	TyrSluSlutleTyrLeulysAsrlysAspl.coAspAlaArqleulbetraAspHisAsp	290	27
136.	AATTOTOTTGGACTTGTAACATCTAATGGACTICCAGAGGTIGAAAAICTITCCAAACGA	901	Db
1. 3	AsnSerLeuGlyLeuValThrSerAsnGlyLeuProgluValGluAsnLeuSerLysAra .	270	γQ
¥	CATGAATGTAATATATAGAGGAGGGGGAAAAATGTFTAIIICAAAAATTITAIAGCIIIIAIG	841	da
269	HisGluCysAssIleAspGluValLysAssValTyrPheLysAssPhelleProPheMet .	250	F
#. 4:	GTAPGAIAGEAAAACAACIAGAAAATGAIACAAGAAIIAIIGAACITCTCTGTAAAAAAA	781	व्य
1. 28 3	AlaArgileAlaLysGlnLeuGluAsnAspThrArgileTleGluValleucystyst).	230	Qy
α	ACAGCTGTTATACCCATTAAATGGTTCAACCTCGAACACCCCAGGCGAGGTCAGAA ACGAAGT	721	Db
t. b., ⋆	ThrAlaValileProlleAsmGlySerProAraThrProAraAraGlyGlmAssAruSer .	210	27
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7,6	GCTANAUGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAGTTAATGGTA	601	Дb
a 4	AlaLysClyCloValLouGlaMotGlaAspAsploaValllosOrPhoclab.cuMetLou	170	0у
Ŝ	ATATCTACTGAAATAAATTCTGCATIGGTGCTAAAAGTTTCTTGGATCACATTTTTATTA	541	Db
£. 4	IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpTleThrPhete.Leu	150	Qy
-E-	CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACCCAGCAGCAGCTAGCAGTTGGAACTTATATATTTTGACACAACCCAGCAGCAGCTAGCAGTTGGAACTTATATATTTTTTTT	481	. Db
14.4	LeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnProSerSerSer	130	Эү
48.	AGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATTGAT	421	
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- 6	TrpThrtAcuPheGInHisThrtAcuGinAsnGIuTyrGlutAcuMetArqAspArqHis 	650 2041
649	ArqLeuAsnThrLeuCysGluArqLeuLeuSerGluHisProGluLeuGluHis II	1981
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SC KI	ProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArqLeuAlaTyrLeu 	610 1921
509	ArqValAsnSorcThrAlaAsnAladbothrdInalaThrSoraIaPhodIngbrdIniys	590
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589	The AldaldaspmetTytleusetProValarqserProLysLysLysLysGlySerThrThr	570
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569	GTyProThrAspHisLeuGluSerAlacysProLeuAspLeuProLeuGjnAspAspHis	550
1800		1741
549 · 1740	LeuAla II pleuSerAspSerProfeuPheAspbeuffetysGInSerLysaspArqGIu 	1881
529	Ashleuth argglumetilelysHisleuGluargGysGluHisargilemetGluSer	510
1680		1621
509	LenAsuLeuLysAlaFheAsp?heTyrLysVallleGluSerPheIleLysAlaGluGly	490
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489	Soy PhrSoy ClinAsidanAspSoyClythrAspLouSoyPheProTypileLeuAsnVal	470
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                                                                                                                                             242 GGAGTATTGGGAGGTTATATTGAAAAGGAAAAAGGAACTGTGGGGAATCTGTATCTTATT 301
                                                                                    182 ATACCAGATCATGTCAGAGAGAGAGAGTTGGTTAACTTGGGAAAAAGTTGATCTGTGGAT 241
                                                                                                                                                                                                      77 ------ ValAspLeuAspGluMetSerPheIhrPheIhrGluLeuGluLysAsulieGlu 94
                                                                                                                 66 | HeProAspHisValArqGluArqAlaTrpLou---
                                                                                                                                                                                                                                  26 ProProProCluGluAspProCluGluAspSerGl\gammaProGluAspLeuProLeuVal(45)
                                                                                                                                                                                                                                                             retinoblastoma gene probe
Patent: EP 0293266-A 1 30-NOV-1988;
RESEARCH DEVELOPMENT FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
A method for detecting the predisposition to retinoblastoma and a
method for detecting a retinoblastoma gene in tumors using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.sapiens DNA for 4.6 kb retinoblastoma gene probe \Delta 0.1444
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40 A	454	435 GluArqLeuSerTleGlnAsnFheSerLysLeuLeuAsnAspAsnIlePheHisMeiSer	ć
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  Onadim, Z.,
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Hogg, A. and Cowell, J
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Molecular mechanisms of oncoceptic mutations in tumors from patients with bilateral and unitateral retinoblastoma
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
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SPLFDLIKQSKDRFGPTDHLESAGPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
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/translation-"MPPKTPKKTAATAAAAAAEPPAPPPPPPPEEDPEQDSGPEDLPL
VRLEFEETEEPDFTALCQKLK [PDHVRERAWLTWEKVSSVDGVLGGY1QKKKELWG1C
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/protein_id="AAB59465.1"
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     515 ATAAAACAGCIGITATACCCATTAATGGTTCACCTCGAACACCCAGGCGAGGCGAGGTCAGAACA 574
                                                 793 IGCTATGIGTCCLFGACIATTTTALFAAACTCLCACCICCCALGTIGCICAAAGAACGAT 852
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                                                                                                   TOPTATOTOPPOPTICIACTATEFIATERAAPTOTCACCTCCCATGTTGCTCAAAGAACCAT 514
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                                                                         1873 GAGAAGGACCAACCATCACCTTGAACCTGCCTCTAATCTTCTCCCGGAATA 1932
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                                                                                                            Praft entry and computer readable a provided by S.H.Friend, 10-FEH-1988
                                                                                                                                                                                                                                                                                                                                                                                                           4600 bp mkNA
Human retinoblastoma associated (RH1) mkNA,
M33647 J02994
                                                                                                                                                                                   Deletions of a DNA sequence in retinoblastomas and mesenchymatumors: organization of the sequence and its encoded protein Proc Natl Arad. Sci. U.S.A. 44 (24), 9050-9053 (1987)
                                                                                                                                                                                                                                                                              Mammalia; Eutheria; 1
1 (bases 1 to 4600)
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   retinoblastoma protein.
Homo sapiens (clone: p4.7k) cDNA to mRNA
                                                                                                                                                  3480530
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                                                                                                                                                                                                                                                              Friend,S H , Horowitz,T M .
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                                                                                                                                                                                                                                             Li, F.P. and Weinberg, R.A.
               /db_xref-"taxon:9606"
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/clone-"p4.7R"
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Local Similarity 94.1%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 PEPCEGGPACHUCCUPGGPPULGCPCTCCTGAGGAGGAGAGAGGAGAGAGGGGCCGG 123
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                                                                     2701 ANACTGGCAGAAATGACTTCTACTGGAACACGAATGCAAAAGCAGAAAAATGAAATGAATAAGC 2760
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ATIGNA FACCIFCAAACAAGGAAGAGAAATGAGGATCTCAGGACCCTTTGGTGGAGACTGTGTGTA 2616
                                                                                                              AAACTGGCAGAAATGACTTCIACTGGAACACGAATGCAAAAAGCAGAAAATGAATGACTAGC 2556
                                                                                                                                                                                                                                       GAAGGATCAGATGAAGCAGATGGAAGCATCTCCCAGGAGAGTCTCAAATTTCAGCAG 2496
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1115 TCGAAATTGGATCACAGCGATACAAACTTGGAGTTCGCTTGTATTACTGAGTAATGAAAT 1174 	1055 TGANGGATATAGGATAN ATCTTTAAANGGAAAATTTGGTAANNY THIGSIAN AGGITATIG III4 	<u>></u> - >		875 AAAGTAACCITGATGAAGAGGGGAATGTAATTGSTGSAGACASASSAGTTGAAGASTAAGAGTGTTA 9×4 [HILLHILLHILLHILLHILLHILLHILLHILLHILLHIL	815 ATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTGAAACACAGAGACACAGACACCACCACCACCACCACCACC	755 AACGATACGAAGAAAFTTATCTTAAAAATAAAGATCTACATGCAACATATTTTTCCAAFC 814 	695 TTATGAATTCTCTTGGACTTGTAACATCTAATGGACTTCCACACGTGAAAATCTTTCTA 754 HIIIHHIIHHIIHHIIHHIIHHIIHHIIHHIIHHIIHH	635 AAGAACATGAATGTAATATAGATGAGGTGAAAAATGIFTATITCAAAAATIITATACCTT 694 	575 GGAGTGCACGGATAGCAAAACAAGTAGAAAATGATACAAAGAATTATTGAAGTTCTCTGTA 634 	515 ATAAAACAGGTGTTATAGGGATTAALGGTTGAGGLGAAGAGGGGGAGGGGGAGGGGAAGAGGGGAGGGGAGAGAG	455 TIGCTATIGT CHOOTTIGACTATETT ATTIAAACTICTCACCTOCCATGTT CCTCAAACAACCAT 514 HTH HTH HTH HTH HTH HTH HTH HTH HTH HTH	395 TATTAGCIAAAGAGGAAGIATTACAAATGGAAGATGATCGGGGGAGITCATTTCAGITAA 454 	GTTCGATATCTACTGAAATAAATICTGCATAGGGGCTAAAAGTTTCTTCTACATCACATTTT	614 TEGGACTCTTCAGCAAATEGGAAAGGACATGTGAACTTATATATTTTGGATCACACTATT 494 342 ATCTACTGAAATAAATTCTGGATTGGATCAAAAGTTTTT 494	342	554 ATACCAGTACCAAAGTIGATAATGCTATGTCAAGAACTGTTGAAGAAAGTATGATGTTGT GT c		342	434 GGGGAAICTGIAICHTAITHLI IIIIIII IIIIIIIIIIIIIIIIIIIIIIIIII	374 AGAAAGTTICATCIGIGGATGGAGTATIGGGAGTTAIAIICAAAAAAAAAA

2254 2593	195 TECCEGAGGGAACATCEATATETCACCCCTGAAGAGTC 	dd 4y
2194 2533	135 TGTCACCARTACCTCACATTCCTCGAAGCCCTTACAAGTTTCCTAGTT 	qu VQ
2134 2473	075 TOTICA IGCAGAGACTGAAAACAAATATTTTGCAGTAIGCTTTCCACGAG 	ОУ
2074 2413	015 TOAAACSTGTTTTGATOAAAAAGAGGAGTATGATTGTATTATAGTATT 	90 47
2014 2353	955 TEAAATTCAAAATCATTGTAACAGCATACAAGGATC 	\$ \$
1954 2293	895 ATTFGGACCAAATTATGATGTGCTCCAIGIAIGGCATAIGCAAAG 	qq
1894 2233	835 TCATCTGGACCCIITTCCAGCACACACCGGCAGAAIGAGIAIGAGIA 	95 \$
1834 2173	775 ALCICCOGCIAAATACACPETGICAACGCCETCTGTCTGAGCACCCAGAATTAGAAC 	96
177 4 2113	715 AGAACCA FEGAAAFCTACCTCTCTTCACTGTTFTATAAAAAAGTGTZ 	4d &5
171 4 2053	TANGGGGGTĀAATTGTACTGGAAATGGAGAGAGACACA - - - - - - - - - - - - - - - - - - -	E 99
1654 1993	595 ATCACACTGCAGCAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAGGT THITTHITTHITTHITTHITHITHITHITHITHITHITHI	441
1594 1933	\$ 35 - RANAAGGACCAACTGATCACCTTGAACCTGCTGCTTGTCCTCTTAATCTTCCTCTCCAGAAR 	dq Vû
153 4 , 1873	475 AATCCCTTHCATGGCTCTCAGATTCACCTTATTTGATCTTATAAACAATCAAAGGA 	9G VQ
1474 1813	415 AAGGCAACTTGACAAGAGAATGATAAAACATTTAGAACGATGTGAACATGGAATGAAT	9d 4&
1414 1753	355 AFGLOCHTAATFFAAAAQCCTFLOATFTTTACAAAGTGATCGAAAGTTTTAT FILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	ÓУ
135 4 1693	295 - GOAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTTCCCATGGATGCT 	£ 9
1294 1633	235 ACAACATITTICATATGTCT/PTAT/GAACT/OAACATITTICATATGTCT/PTAT/GAACT/OAACATITTICATATGTCT/PTAT/GAACT/OAACATTITICATATGTCT/PTAT/GAACTATAAACATTITICATATGTCT/PTAT/GAACTATAAACATATTICATATATATAATAAACATATAAAAAAAA	96
1234 1573	175 CCATGCTTAAATCAGAAGAAGAAGAACGATTATCCATTCAAA FILLIGHTIILIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	qq

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215 AAAGCTGGAAGCAAAGTATAACCATATGATACTATCATACTACTGAAACAGATTTCATA	2915 CTGTCTGACTACTTTGCCTTCTTTGTAGCAIAIAGGIGATGTTGCTGTITTATT [HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	2675 TATGGCCACATITAATAICTICAGGTCTITITGIGGATATAAAAIGTGCAGAIGCAATIG [HIH]HIH]HIH]HIH]HIH]HIH]HIH]HIH]HIH]HIH	255 TIGCCAACACCACACAAAATIGACTICCACAGATICAAGATICTAAGATTAATATATATATATATATATATATATATATATA
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CTATGTGTCCTTGACTATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCATAT		42 AFCTACTIGAAATAAATTICTGCATTGGTGCTAAAAGTTTCTTGGGTCACACTTTTTTTA 88 TCGGTGCTACACATTGTGTGGTGCTACACACTTTCTTGGGTCACACTTTTTTTT	CENACTO E L'AGENABA L'EGGABAGGACA EGTGABACT ATATATATATAGACACAGACACTO			404 GGAATCTGTAFCTTTATTGCAGCAGTTGACCTAGTCGA		184 THATGTCAGAAATTAAAGAFACCAGAFCATGTCAGAGAGAGAGAGGTTGGTTAACTTGGGAG 243 	124 GAGGACCTGCCTCTCGTCAGACTTTGAAGATTTGAAGAACAGAAGAACCTGATTTTACTGCA 183 H	64 CONTROL ACCIOCOCOCOCOCOCOCOCOCOCOCAGAGGACCAGAGCAGACAGCAGACAGCAGACAGCAGACAGCAG	KBSBSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	Ouery Match 92.5%; Score 3096.2; DB 6; Lenath 4597; Best Local Similarity 94.0%, Fred. No. 0. Matches 3338; Conservative 0; Mismatches 3; Indels 210; Caps 3;	NI Ce	Dryja, L Human Dr Patent:	<u>\$</u>	1 Sequence 1 from Fateut EF 0259031. 105411 105411.1 G1:591083	108411	
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1537 GAAGGACCAACTGA ECACCTTGAATCEGCTTGTCCTCCTTAATCTTCCTCCCAGAATAAT 1596	1477 TOCCTTGCATGCCTCCAGATTCACCTTTATTTGATCTTATTAAACAATCAAAGAACGA 15 0 	* 1417 GGCAACTTGACAAGAGAAATGATAAAACATTTAGAACGATGGAACATCAAGCATCAATGAA 1436 	* 1357 GTGCTTAATITAAAAGCCTTTGATTTTTA*'AAAGTGATGAAGTHTTATCAAAGCAGAA 1416 	1297 AGAAGTACATCITCAGAATCITGATICTGGAACAGATTITGICTIIFC CAIGCAIICITGAAI 1856 	1237 AACATETETCAFAFOTCITTATTGGGGGGCGCTCTTCAGGTGGTAATGGCCAATATATACT 1256 	1177 ATGCTTAAATCAGAAGAAGAACGATTATCCATTCAAAATTTTAGCAAACTTCCAAACTTCCAAACGACTAAACTACCAAAACTACCAAACTACAAACTACAAAAATTTTAGCAAAACTACCAAAAACAACTACCAAAAAATTTTAGCAAAAACTTCCAAAAACTACAAAAACAACAACAACAACAA	1117	1057 AAGGATATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTGTGTC 1116 	997 1198	937 AAC 111 1138 AAC	877 AGT 1078 AGT	817 GAT 111 1018 GAT	757 GATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGTAAGATTATTTTTGGATCAT HIG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	697 AIGAATHCICITOSACTEGIAACATCIAAIGGACHECAGACRIBGAAAAICHICIAAA 796 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	637 GAACATGAATGTAATATAGAATGAGAGGAGAAAAATGTTTATTTCAAAAAATTTTATAGACTTTT 696	577 AGTGCACGGATAGCAAAACAACTAGAAAAAAAAAAAAAA	517 AAAACAGCIGTTATACGCATTAATGGTTCACCTCGAACACCCAGGCGGGGGGGG	

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ATGGATACCTCAAACAAGGAAGAGAAATGAGGATCTCAGCACCTTGGTGGACACTGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACACCAACAAAABTGACTECAAGATCAAGATCTTAGTATCAATTTGGTGAATCATTC
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                                                                                                                                                                                                                                                                                                                                                    AAAAAAAGTGCTGAAGGAAGCAACCCTTCTAAACCACTCAAAAAAACTACCCTTTCATATT 2436
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                            261 TGGAGTATTGGGAGGTTATATTGAAAAGAAAAAGGAAGTGTGGGGGAATCTGTATGTTTAT
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Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
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1062 TATAGGATACATCITTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGTTGTGTGGAAA1 :1:1
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945 TATAGGATACATCTTTAAAGAGAAATTTGCTAAAGCTGTGGGACAGGGLLGLGLGLGAAA.
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Xu,H.-J., Hu,S.-X. and Benedict,W.F.
Broad spectrum tumor suppressor wence
tumor suppressor gene therapy
Patent: US 5912236 A 1 15-JUN-1999;
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ATCTG 	1782 - GCTAAATACACTTTGTGAACGCCTTCTGTCTGAGCAGCGCAGAATTAGAACATATC 	
CTCCC	1722 - AFTSAAATSTACCTETESTFICACTGT FTTATAAAAAAGTGTATEGGGFAGGGTAT 	
AAGCC NAGCC	1662 TOTAAAT FOTACTONAAA IONAGAGACANAAGNAAGCTGAGGCTTTCCAGACCCAG 	. .
0000 0000	1602 TOPAGYAGATATGTATCTTTCTCCTGTAAGATCTCCAAAGAAAAAAAA	~ -
ACAC	1542 ACCAACIGAICACCITIGAATCIGOTTOTOS ICCTAATCITCCTCTCCAGAATAATC 	рь — I
AAGG AAGG	482 TOCATOJCT CTCAGATTCACCTITAT LIGATCTIATTAAACAATCAAAGGACCGAG 	
CCCT	4.22 - CTTGACAGAGAGAATGATAAAACATTTAGAACGATGTGAACATGGAATGAAT	ОУ 1 РЪ 1
GCAA	1462 TAATTI AAAAGYYTTEGATETTIACAAAGIGATOGAAAGTI ITAICAAAGCAGAAA 	
TGCT	1902 FACA POTOAGAA POTTGA EFOTGAAA GA ETTG FOTTT TOCCA TGGATTG TGAA FG 	L .
GAAG	1242 TEFFOATATGTCTTTATFGGCGTGCGCTCITGAGGTTGTAATGGCCACAFATAGCA 	
AC A I	ITB2 - LAAALCAGAAGAAGAAGAACBALCATEGATEGAAAACTETTAGGAAAGTEGTGAATGAGA 	1 AO
ATGCT	1122 - TÖĞA EVAÇA GATAÇAA ÇALEĞA AÇIL EĞA ÇIL EĞER ERÇEKTIĞI A FIAÇEĞAĞI AATIĞĞA I EÇE 	

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Xu,H.-J., Hu,S.-X. and Benedict,W.F.
Ku,H.-J., Hu,S.-X. and Benedict,W.F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1722 ATTGAAATCTACCTCTTTCACTGTTTTATAAAAAAGTGTATCGGCTAGCCTATCTCC; 2741
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                                                                                            1392 CAAAA9CAT9GTAACAGCATACAAGGATCTTCCTCATCCTGTTCAGGAGACATTCAAACC 1444
                                                                                                                                                                               1962 CAAAATCAFFGTAACAGCAFACAAGGATCTICCTCAFGCTGTTCAGGAGACAFFCAAAACS 2 2
                                                                                                                                                                                                                                                                                 1902 CCAAATTATCATGTGTTCCATGTATGGCATATGCAAAGTGAAAGAATATAGAGCTAAAAT Ey61
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316	* 4102 ATATTATTAGAAAFTAGAAAAAAATTAGTAATTTTACACATT	υY
25	4042 AARGYAATERGATEGACTGGCCCATEGACGGAAAATTATGGTGAAGTGTTGTGGGAAAAAT HILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	£ 5
30	2982 ATGTATATTTTTTAATTTAACATGAACACCCTTAGAAAATGTGTCCTATCTAT	5 5
29 37	7 2922 ACTACTETECCE TOTTTIGTAGCATATAGGIGA IGFT IGCIC FIGTT ITTATTAATTI 	E 9
4 3	2862 PREPERTA PRATAGHAGIAA PAGEEN TAGAGHAGGGGGGGCOGTO ALAACCCAGGCCOGTO LILIHAH HALLIHAH HALIHAH HALLIHAH HALLIHAH HALLIHAH HALLIHAH HALLIHAH HALLIHAH HALLIH	₽ 9
4 2 9 8	2802 TAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTT 1	£ 5
55	2742 GATTOCTAAGCCACTTGAAATGTTAGTCATTGTTATTATACAAGATTGJ 	£ 5
27 61	2682 ACATTTAATA ICTTCAGCTCTTTTTGTGGATATAAAATGTGCAGATGCAAT 	B 6
26 67	26.22 CTROATFONTFOTCTCTCACAGATGTGACTGTATAACTTTCCCAGG 	<u> 5</u>
26 73	2562 TAPOTOAARCAAGGAAGAGAALGAGGALOTGA 	E 68
79	2502 GECAGAAA DAG FECTACTOGAACAGGATGGAAAAGGACAAAA BGAACGATAGA 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 11 852 GECAGAAATGACTTCTACTCGAACAGGAATGCAAAAAGGAAAAATGAATG	P 95
00 K ∷n ∪n	2442 ATCAGATGAAGCAGATGGAAGTAAACATCTCCCAGAGAGAG	£ 5
24 91	2382 ANG DOTGAAGGAAGCAACOCTOC FAAACCACTGAAAAACTACGCTTTGA 	₹ <i>5</i>
23 97	2/22 FICTGAGAAAFFYCAGAAAAFAAATCAGAFGGYATGTAACAGCGACGTGTGC 	₹ Ş
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                                                                                                                                                                                                                                                                 405 AGCTGTTATACCCATTAATGGTTCACCTCGAACACCCCAGGCGAGGTCAGAACAGGAGTGC 464
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762 GGAAGAAATTTATCTTAAAAAATAAAGATCTAGATGCAAGATTATITTTTGGATCALGATAA 621
                                                                         702 TTCTCTTGGACTTGTAMCATCTAATGGACTTCCAGAGGTTGAAAATc111c1AAACGATA 761
                                                                                                                                                                                       4.65 ACGGATAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAAGTCTCTGTAAAAACAACA 5.24
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                                 TTCTCTTGGACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAAATCTTTCTAAAACGAAA 444
                                                                                                               TGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTTTATGAA SKI
                                                                                                                                                                                                                                                                                                     AGCIGITATACCCATIAATGGITCACCICGAACCCCAGGCGAGGICAGAA AGGAGIGC 581
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Broad spectrum tumor suppressor genes.
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Patent: US 6074850-A 3 13-HHN-2000;
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Antelman,D., Gregory.R.J. and Wills,K.N.
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                                                 ACAAACTOOCAGAAATGACTIVEWACWEGAACAGGAAWGGAAAAGGAGAAAATGAATGATA 2554
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 TCANANGANGTGCTGANGGANGCANGGCTGANAGGARIGAMMANAGTAGGCTTTGNTN 2434
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CANJI INC
ON Unidentified
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PD 21-MAR-2001
PF 13-NOV-1997 JP 199522958
PR 15-NOV-1996 US 08/751517,14-FEB 1997 US 08/NOI
DOUGLAS ANTELMAN, RICHARD J GREGORY, KENNETH N WILLS PC CC Strandedness Single;
CC Topology: Linear;
FT Source JOSESSA / Organism-'Unidentified'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 2994)
                                 /organism="unidentitied"
/db_xref="taxon:32644"
                                                                                            Location/Qualitiers
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                  593 q
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Hest Local Similarity

72.7**8**; 92.7**8**;

Score 2433.8; Pred. No. 0;

DH 6;

Length 2994

Ouery Match

	40 40	B 6 B 6	da da Ada	40 40 40 40	4 A	ψ Φ b	00 dq	Ma Db
695 TTATGAATTCTCTIGGACTTGTAAVATCTAATGSACTTCAGAGGTTGAAAATCTTTCTA 754	575 GGAGIGCACGGAIAGCAAAACAACIAGAAAATGAIACAAGAATIATIGAAGTTCTCTGTA 634 [455 TGCTATGTTGCTTGACTATTTTATTAACTCTCACCCCATGTTGCTCAAAAACAC 514	342ATCTACTGAAATAAATTCTGCATTGGTGGTAAAGSLITCITTGGATCACATTT 394	342 554 ATACCAGTACCAAACTTGATAATGCTATGTCAAGACTCTTGAAGAAGTATGATGTGATGT 613 342 341 614 ITGCACTCTTCAGCAAATTGGAAAGGACATGTGAAGTTATATATTTGACACAAGCCAGCA 673	434 REGERANT CHETTATTE CAGCAS PRESENTE ACTE AGARGAGAT GROUP GETT CACT TO THE ACTE AGA AGARGAGAT GROUP AGA AGA AGA AGA AGA AGA AGA AGA AGA AG	ANAAAGPETGATGTGAGGAGTARTGGAGGTEATATTGAAAAGAAAAAGGAACTGT 	122 CHARRANCTGCCTCTCGGTCAGGCTTGAGTTTGAAGAAACAGAAGAAGACCTGATTTTACTG 181	Matches 2652: Conservative 0; Mismatches 2; Indels 207; Gaps 2 GCGTCATGCGGCGAAAACCCCCCAAAAACCCCCCAAAAACCCCCCGAAAACCCCCC
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1114 ATC 835 TCA 1111 1174 TCA 895 ATT 234 ATTT		874 GAG 874 GAG 595 ATC 934 ATC	V 44 TU 44 T	634 GCA .355 ATG .11+ 694 ATG	G ACA	1115 TOGAAATTOGATOACAGOCATACAAACTTOGAGT COCTTGTATTACCGAGTAATGAAATTIGTAATTOGAATTAGAAACTTOGAATTOGAATTOGAATTOGAATTOGAATTOGAATTOGAAATTOGAATTAGAAACTTOGAATTAGAAAACTTOGAATTAGAAAACTTAAAAACTTAAAAACTTAAAAACTTAAAAACTTAAAAACTTAAAAATTAGAAAACTTAAAAATTAAAAAAAA	995 ATGTRATTTCCTATTETAACAACTGCACAGTGAAHCCAAAAAGTATAACTGAAAAAAA 111111111111111111111111111111	AAA NAA TGA

Query Match 72.7%; Score 2433.8; DB 6; Length 2994; Rest Local Similarity 92.7%; Fred. Ro. 0; Matches 2652; Conservative 0; Mismatches 2; Indels 207; Gaps 1;	FEATURES Location/Qualitiers Source 12994 /ordanism="unknown" HASE COUNT 974 a 618 c 593 g 809 t	AUTHORS Shopard,H.Michael. and Wen,S.Fen. 1111E Characterization of a novel anti-pl10.sup.RH monoclonal antibody JOURNAL Patent: US 5710255 A 2 20-JAN-1998;	Unknown. M Unknown. Unclassiti	ce 2 from patent US 5710255. .1 G1:3209762	RESULT 15 181465 - 181465 - 2994 bp DNA libear PAT 10-JUN-1998 Locus IR1465 - 2994 bp DNA libear PAT 10-JUN-1998	Oy 2615 TACACCTCTGGATTCATTGTCTCTCACAGATGTGACTGTAI 2655 [] [] [] [] [] [] [] [] [] [] [] [] [] [- QY - 2555 GCATGGATAGGTAAAGAAAGAAGAAATGAGAGATGTGAGGAG	UY 2495 AGAAACTIGA AGAAATGA TITOTTACTIGGAACACGAATGCAAAACCACAAAATGAATGATA 2554 	UY 24.35 TTGANGGATCNGATGANGCNGATGGANGTANACATCTCCCNGGAGAGTCCANATTTCNGC 24.94	UY 2375 TCANANGANGGCTGANGGANGCANGCCTCTANACCACTGANANACTAGGCTTTGATA 2434	UY 2315 TORGGACTICTGAGAAGTICCAGAAAATAAATCAGATGGTATGTAACAGCGACGTGTGC 2374 {	OY 2255 TGCYANCANAAAAAAAAAAAACAACTO'AAGATCAAGAATCITAGTATCAATTGGTGAATCAT 2314, 	OY 2195 TEPOTERANARANATOTATATITONOCOLIGANGNGTOCATATAANATTTONGANGGTO 2254 	OY 2135 TRICACCAAFACCICACAFICCECGAACCCEFFACAACFICCEGAGTECACCCEFFACGA 2194 [HILLHILLHILLHILLHILLHILLHILLHILLHILLHIL	OY 2075 TOTTOATOMANAVTAAAAACAAATAITTISGAGTATSOTTGGAGGAGASGGGGGAGGT 2134 	OY 2015 TSAAA SITSITTTSATSAAASAASAASASITAISATTOTAITATAITA	Db 2394 TTAAATTCAAAATCATTCTAACAGCATACAAGAATCTTCCTCATGCTGTTCAGGAGAGACAT 2353
Oy 815 ATGATAAAACTGTTCAGACTGATTATAGACAGTTTTGAAAACAGACAG	755 AACGATACGAAGAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTGGATC	Oy 695 HAIGAAHGICHGGACHGIAACAHGIAAHAGAGHGGAGHGAAAAHCTTTCTA 754 HILLIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH		Qy 575 GGAGTGCACGGATAGCAAAACAACTAGAAATGATACAAGAATTATTGAAGTTCTCTGTA 644	Oy 515 ATAAAACAGCTGTTATAGGCATTAATGGTTCAGCTGCAACACCAGGCGAGGTCAGAACA 574 	Qy 455 TGCTATGTGTCCTTGACIATTTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAACCAT 514	79 TATTAS TAAASSAAAGTATTA AAAISSAAGATGATTGGTGATTTCAGTTAA 454	Oy 342ATCTACTGAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATGACACATTT 894 [QY 342	QY 342	Db 494 AGCTACAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTAAAAAAAA	Gy 302_GGGGAATCIGIATCTTATTGCAGCAGTTGACCTAGTGGA	9y 242 AGAAAGIIRCALCIGIGGAIGGAIGTATTGGGAGGTTATATTCAAAAGAAAAAGAAAAG	Oy 182 CATTATGTCAGAAAFFAAAGATAGCAGATCATGTCAGAGAGAGAGAGACACCTTGGTTAACTTGGT 241 	Qy 122 GGGAGGACCIGOCTCTCGGICAGGCIIGAGIIIGAAGAAACAGAACACGAIITTACTG 181 	Gy 62 AND CONTRACTOR ACCOUNT	5b 134 GCGTCATGCCGCCAAAACCCCCGGAAAAAACGGCGGCGCCGCCGCCG

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	GPATGRAFAPYTCAAACAAGGAAGAAAATGAGGAAFCTCTCAAGAACTTGGGACACTGTG 2753 TACACCTCTGGAFFCATTGTCTCTGCACAGAGATCTGTAT 2655	GCATGGATACCTCAAACAAG3AAGAGAAATGAGGATCTCAGGATXCTGGGGGAXACTGTG 2614	AGAAACTICICAAAATIGACTICTACTICGAACACGAATIGCAAAAGCAGAAAATICAAATICATA 2893	AGAAACTGGCAGAAATGACTTCTACIUGAACACGAAIGCAAAAGCAAGAAAANAISAAISAAI 2154	TEGANGATINGATIGANGARA PRANAGIANAN'A POPON ANGANGNETICANATTONING - 28 (4	THGAAGGATGAAGGATGAAGGAGATGGAAGTTAAACATGTCCCAAGGAGAGTCCAAA1111CAGC 2494	TCAAAAGAAGTGCTGAAGGAAGCAACCCTGCTAAACCACLGAAAAAAAACIACGCIII15ATA 277	TCAAAAGAAGTGCTGAAGGAAGCAACCCLCCTAAACCACTGAAAAAAACTACGCTTTGATA 2434	TOGGGACTTCTGAGAAAGTTCCAGAAAATAAATCAGATGCTAACGTAACAGCGACCGTGTGC 2714	TCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTAAGAGCGGCGCGTGTGC 2 < 74	TGCCAACAACAAAAATGACTCCAAGATCAAGAATCITAGTATCAATTGGTGAATCAT 265	TGCCAACAACAAAAAATGACTECCAAGATCAAGAATCTTAGTATCAATTGGTGAATCAL 2314	ITCCTS/ANS/ATATOTATATTTC/ACCCCTS/AA/SAGTCCATATAAAAATI FCA/SAA/GTC 259×	TTCCTGGAGGGAACATCTATATTICACCCCTGAAGGCCCATATAAAATTICAGAAGGCC 2254	TGTCACCAATACCTCACATTCCTTCGAAGCCCTTACAAGTTTCCTAGTTCACCCTTACGACCCTTACGAGCCCCTTACAAGCCCCTTACGAGCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCCCCTTACAAGCAGCAGCAAGCA	TGTCACCAATACCTCACATTCCTCGGAAGCCCCTIACAAGIITCCTAGIICACCCCTTACGGA 2154	TCTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCAGCAGGCCCCCTACCT 247	TCFTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGCCCCCTACCT 2134	TCAAACGTCTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCTATAAACTCGG 241	TCAAACGTGTTTTGATCAAAGAAGAGGGAGTATGATTGTATTATAGTATTCTATAACTCGG 2074	TTAAATTCAAAATCATIGIAACAGCATACAAGGATCTTCCTCATGCTGTTCAGGAGAGACAI 2354

Search completed: January 17, 2003, 18:09:53 Job time: 5609.08 sees

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Command line parameters:

MODEL trame: _p2n.model - DEV-x1h

- MODEL trame: _p2n.model - DEV-x1h

- CFGP2 | TUSE: __scal_USA-125.42; nort_120.120.03 | 1521.67_24.097.4FF_porty fast:_1 174.67

- CDB-GenEmb1 - QFMT-Lastap - SHEFIX-ree - MINMATCH-0.1 - LOOPCL-0 - LOOPEXI-0

- CNITS-bits - STAFT-1 - FND--1 - MATPIX-blosun62 - TPANS-buman60.cd1 - LIST-45

- DOCALIGN_200 - THE_SCORE - PORT - THE_MAX-100 - THE_MIN-0 - ALIGN-15 - MODE-LOCAL

- OUIFMI-pto - NURM-CXT - HEADSIZE-500 - MINLEN-0 - MAXIEN-200000000

- USER-USO9026454_actal_CXL_12660__STAFE-500 - MAILEN-20000000000 - NURM-CXT - MACSONES-C - WALL - LOORDOC - THE - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC - THE - CARDOC 
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em_htqo_other:*	em_htqo_mus:*	Ξ	om_sy:*	em_htq_vrt:*	em_htq_mam:*	em_htq_rod:*	em_htq_plu:*	em_htq_mus:*	om_htq_other:*	em_htg_inv:*	em_ht q_hum:*	** - A - A - A - A - A - A - A - A - A -

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ARROSH 965 ARROSH 965 ARROSH 965 ARROSH 965 ARROSH 81 HUMRHARA HUMRHARA HUMRHARA 109489 ARLAA787 HUMRHAR 1109469 ARLAA787 ARROSH 96 ARROSH 1118497 ARROSH 11

ALIGNMENTS

RESULI 1

Db 739 GCTAAMGGGGAAMGTATTAGAAATGAAATGATGTGATTGATT	Oy 132 AlaLysdlydlavalloadisMotolnAspAspLoaVallleSerbbeOlnLeuMetLeu 151	OV 113SerThrGluileAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 131	Db 619 CTCTTCAGCAANTIGGAAAGGACATGTGAACTTFATATATTTTACAACGAACGGAGGAGTTCC 578	11	· -	Db 499 CAGAAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAAGAAATTGATACC 558	112	439 AICHGIARCTTTATHGCAGCAGTHGACCTAGATGAGATGT	ACESTS AND ACCOUNTS OF THE TOTAL TOTAL ACCOUNTS AND ACCOUNTS OF THE TOTAL SECTION OF THE TOTA	Oy 81 ValSerSerValAspGlyValLeuClyClyTyT1leClnLysLysCluLeuTrpGly 100	Qy 61 CysGlpLysLeuLysIleProAspHisValArqGluArqAlaTrpLeuThrTrpGluLys 80	Qy 41 ASPLeuProLeuValArqLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu 60	_		1 Met.ProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaA	-09-026-459A-43 (1-859) x ARO91965 (1-2994)	cal Similarity: 92.46% Mismatches: atch: 99.84% Indels: 99.84% Gaps.	Pred. No.: 1.21e-316 (ength: 2994 Score: 4401.50 Matches: 858 Percent Similarity: 92.468 Conservative, 0	HASE COUNT 974 3 EFE C 544 3 828 t Alignment Scores:	RES Location/Qualifiers source 12994 /organism="unknown"	REFERENCE: I (bases I to 2994) AUTHORS Lee,WH. and Lee,E.YH.P. TITLE Retinoblastoma gene cancer suppressor and regulator JUODNAL Palept: US 5998134-A 4 67-per-1999.	Unknown. M. Unknown. Unclassified.		AR091465 LOCUS AR091965 2994 bp DNA linear PAT 08-SBP-2000 DEFINITION Sequence 4 from patent 05 5998134.
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Lee,W.H., Shew,J.Y., Hong,F.D., Sery,T.W., Demoso,L.A., Young,)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retinoblastoma protein; retinoblastoma susceptibility protein Homo sapiens retinoblastoma cDNA to mRNA.
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PROGNIY ISPLKSTYK (SEGLETETKM) FRSETLUSETE FERTERSTYKFESSELE
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/cell_line="retinoblastoma cell line y79, and normal
retinoblastoma cell line"
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/db_xret="GI:190963"
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271	TyrCluClulleTyrLeuLysAsnLysAspLeuAspAlaArqleuPheLeuAspHisAsp	252	PF 23
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231	HISGINCYSASnIleAspGlnValLysAspValTyrPheLysAspPhcIleFroPheMet	212	dd
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211	AlbargileAlaiysGlniepGlbasnaspThrarglleIleClbValLeuCysiysGls	192	ob
978			V
191	ThralavallleProlleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSer	172	40
918		859	
171	CysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGluProTyrLys	152	95 A
858		799	
151	AlalysGlyGluVall.euGlmMetGluAspAspleuVallleSerPheGlmLeuMetLeu	132	op
798		739	Ad
131	SerThrGlulleAsnSerAlaLeuValLeuLysValSerTrpf)eThrPheLeuLeu	113	ОУ
738		679	Db
678	CTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTTGACACAACCCAGCAGTTCG	619	рb
112		112	Ş
618	AGT AGGAAAGT TGATAATGGT ATGT GAAGAGTGTT GAAGAAGTATGA TGTATTEGGA	559	E &
558	CAGAAAAACATAGAAATCAGTGTCCATAAATTCTTTAACTTAGTAAAAGAAAATTGATACC	499	DP.
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80	CysClnlysLeafysHeProAspdisValArqCluArqAlaftpLeafbrfrpCluLys	61	40
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60	AspLeuProLeuValArqLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu	41	90
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40	ProAlaProProProProProProProGlud (aspProGlud InaspSerGlyProGlu	21	B &
258		199	
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Human retinoblastoma associated (RH) mRNA, complete cds.
M3647 J02994
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Homo sapieus (clone: p4.7k) cDNA to mRNA
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Oncogeric point mutations in exc. 20 of the RES game in
showing incomplete penetrance and mild expression of the
rethroblastoma phonotype
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                                                                                                                                                 Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
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Mutation data provided by Dr. B.L.Gallie
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<pre>/note="Tumor Gos537 bilateral trameshift mutation causing promature stop.: 600 ll8-734" /* itation [5] /*replace "c" 638676 /pene-"RBI"</pre>	/ Citation [5] / Citation [5] / Teplare-"ta" / 4-ne-"RB] "	/number-4 537. 542 /dene-"RBI" /note-"Tumor (20856) unilateral trameshift mutation causing	/replace-"ca" 518647 /dene-"Rist" /dene-"Rist	506509 /gene-"MHH." /note-"MHF64 bilateral familial deletion mutation causing /premature stop"	402517 Agene="R61" Znote="R00-118-734" Znumber 4	275 401 /detie="RB1" /noto="600 118-734" /numbet=2	20408	TANASTOATSAFOTOKRUKSTSISLEPYKKYYRLAYLIRLAYLICERLISEIRELEHTIWT LEOHTIONEYELMKORHLDO IMMOSMYGTOKVKNIDLKEKTIVTAYKOLPHAVQETEK KVILIKEEKYTOST I VEYNISSEMOKIK IN LIQVAS PREPTI SPITRI PRSPYKEPSSELK I PRGNIYTSPIK KSPYKISESTIK IN LIQVAS PREPTI SPITRI PRSPYKEPSSELK I PRGNIYTSPIK KSPYKISESTIK KOMVONSO RVIKRSAFOSKNIFATIKKIRFULBGSUFADGSKHURGESKEOKTAEMISTETEMOKO KMNOSMOTSNKEEK"	INTERVIENDA DE LE CONSONES EN LENGANDA DE MANGRENGMENDALE DE CLE MACVELINE IKK.SEPRELLKEPKENDA EN RESPONESSARIA KOLENDER LIEV LOCKEHEONI DEVKNYFENE I PENNSLGLVTSNGLPEVENLSKRYEET VLKNKDLDAR LELDHDKTLOTISS IDSEPTOPPEKSNI DEFUNDI PPHTPVPTVMIT LOQIAMILLISA SDOPSENL I SYFNN' I VNEKES HAKKNALGY EN KEKFARAVGOGOVELOSORYKLOV RILYYKVMESMLKSEEERLS IONESKLLNDNI FHISLIACALEVVMATYSRSTSONLDS GTDLSFPM LINVLINIKAF DEFYKV LESE KARGNLI KEMINHER CHRITHER IMESLANISD SPLEDLIKOSKOREGETDHILESACPLINLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS	/ Notice Ref / Product = "rot inoblastoma Suspectibility protein " / Product = "rot inoblastoma Suspectibility protein " / Product = "rot inoblastoma Suspectibility / Product = "rot "rot Ref / Rot Rot "rot "rot Rot / Product "rot "rot Rot / Product Rot Rot / Product Rot Rot / Product Rot / Product Rot / Product Rot / Product /note "600 118 734" /note = 600 118 734" /number = 1 138	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	E mail: brendashatiz.eric.on.ca. Localion/Qualitiers 1. 4839 /ordanism "Homo sapions" /db_xret="taxon-9606" /map="13q14.2" 1. 4839	
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Gregory,R.J., Wills,K.N. and Maneval,D.C.
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                                                                             Fyr6laClu1.1cTyr1.ca1.ysAsn1.ysAsp1.caAspA.laArq1.ca6bc1.caAspH1.sAsp. 271
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Draft entry and computer readable copy of sequence in [1] rind() profided by R.Bookstein, 27-APR-1987.
                                   3413073
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                                                                                                       Molecular mechanism of retinobiastoma gene inactivation
                                                                                                                                           Lee, E.Y., Buckstein, R., Young, L.J., Lin, C.J., Eosenteid, M.o.
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                                                                                                                                                                                                                                                                          Lee
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                                                                                        retinoblastoma cell line Y79
                                                                                                                           Lee, W.H
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                                                                                                                                                                                                                                                      Human retinoblastoma susceptibility gene: cloning, identification,
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A FC F GTATC FT FALTEGYACGAG FT GAGG FAGATGAGATGTCGT FGAGTTFACTGAGGTAC
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SPLEDLIKOSKDREGPTDHLESACPLNLPLONNHLAADMYLSFVRSPKKKGSTTRVNS
TANAETOATSAFGIOKPLKSISISLFYKNVYRLAYLRUNTLCERLLSEHPELEHLIWT
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AAGAACATGAA TGTAATATAGAGGTGAAAAATGTTTATTTGAAAAATTTTATACCTT 1032
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exon	ехоп	variation						CDS	exon	gene	FEATURES Source		COMMENT	JOURNAL MEDLINE MEDLINE	REFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL MEDITINE	TITLE JOURNAL MEDIANE PUHMED
/no.ce	/citation=[5] /replace="1" 275. 401 /gene="RBI"			RLYPRVEESMLKSEEERUS IQNESKLLNDNIFIINSLLACALEVVMATYSERSTSONLDS GTDI SFPWIL INVLNIKAFDFYKFIESFIKAEGNLTPEMTKHLEPCEHPIMESLAMLSD SPLFDLIKQSKDREGPTDHLESACPLINLPLQNINHTAADMYLSPVESPKKKGSTTRVNS TANAFTQA ISAFQTOKPLKSISI.SLFYKKVYRLAYLRI.INTLCHRLLSEHPELEH I IMT LFOHTLQNEYELMKDRHLDQIMMCSMYGICKVKNIDLKFKII IVTAYKDLPHAVQETFK	LESKLERIGELITLIQESSISTEINSALVKVSMITTELLAKGGVLQMEDDLVISFQL MLCVLDYEIKLSPPMLLKEPYKTAVIPINGSPPTPRAGNESAPIAKQLENDTRITEV LCKEHRONIDEVKNYVTSKNE IPEMNSIGIATSNGLPEVENISKRYEEIYLKNKDIDAR LEIDHDKTLÖIDS IDSFETQRIPRKSNIDEEVNYIPPREPVRTVMNTIQQUMMILNSA SDOPSENLISYFNNCTVNPKESILKKVKDIGYIF NEKEAKAVGGGCVEIGSOKYKLÄV SDOPSENLISYFNNCTVNPKESILKKVKDIGYIF NEKEAKAVGGGCVEIGSOKYKLÄV	/db_xref-"GD8:G00-118-734" /translation-"MPPKTPRKTAATAAAAAEDPAPPPPPPEDPEGDSGPEDLPL /translation-"MPPKTPRKTAATAAAAAEDPAPPPPPPEDPEGDSGPEDLPL VRLEFERFEREPPFTLOCKLKI FLUVERRAWLIWEKVSSVLOVLOGY JOKKKELWGLC IFIAAVDLDEMSFTFTELOKNIEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA	<pre>/codon_start=1 /product="retinoblastoma suspectibility protein" /protein_id="AAB59465.1" /db xref="G1:79395"</pre>	/note-"G00-118-734" /number-1 138 2924 /gene-"KHI"	/gene="RH " 274 	/organism-"Homo sapiens" /db/xrel-"Laxvu.3606" /map-"l3ql4.2" 1 483g	E-mail: brenda@hatiz.cric.on.ca. location/Qualifiers 14839	FAX: 416 813-4989	Mutation data provided by Dr. B.L.Gallie, Hospital for Sick Children 555 Univ. Avc. Forento ONT W5G 1X8	Partial inactivation of the PP groduct is a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors encogene 9 (5), 1321-1326 (1994) 94203660 8152792	8446255 846255 6 (Siles) Cowell,J.K. and Kaye,F.J.	5 (sites) Hogq.A., Bia,B., Onadin,Z. and Cowell,J.K. Molecular mechanisms of oncogenic mutations in tumors from patients with bilateral and unilateral retinoblastoma Proc. Nati. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993) 4348771	Mechanisms of oncompensis in parliants with familial retinoblastoma Br. J. Cancer 68 (5), 958–964 (1993) 94031584 8217609
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                                                                                                                                 Draft entry provided by
                                                                                                                                                                                                                                 Li,F.P. and Weinberg,R.A.

Deletions of a DNA sequence in retinoblastomas and mesenchymal tumors: organization of the sequence and its encoded protein
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/close-"p4.7R"
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                                         544 TOGATEATOTAC EGAAATAAATTOOTGGATTGGTGCTAAAAAGTTTCTTGGATCACATTTTTTA 603
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SPLFPI IKOSKUPFGPTDHLESACPLNLPLONNHFAADMYLSPVRSPKKKGSTTRVNS
IANAETOATSAFOTOKPLKSTSLSL-YKKVYRLAYLRUNTLCERLLSEHPELEHTIWT
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		784 AGTOCACOGALAGCAAAACAACTAGAAAATGATACAAGAATTATTGAAGTTCTCTGTGAA 843 	5 Vy
	Db Oy	724 AAAACAGCIGITATACCCATTAAAGGTICACCIGGAACACCCCAGGCGAGGGAGGTCAGAACAGG 783	Db Vy
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	AAAATTTATACCTTTT 903 	844 GAACATGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAATTTTATACCTTTT 	96 AA
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	JOGCEAGGICAGAACAGG 783 	724 AAAACAGCIGTITATACGCATTAATGGTTCACCTGGAACACGCGAGGGGAGGTCAGAACAGG 	dg vy
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	TETECATETCAGETAATG 663	604 - TEACCTAAACCCCAACTATTACAAATCCAAGATGATCTGCTGCTGATTTCATTTCAGTTAATG 	9- 0-y
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3538 TTAFFGAFACT 3548
                                                            3544 ITATIGATAGE 3554
                                                                                                                      3478 CAGAATGTAAAAGAACTTACTGATTATTTTCTTCATCCAACTTATGTTTTAAAAGAACGAGGA 3537
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1 (bases 243 to 4740)
Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Show,J.Y. and
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  Conservative
                                                                                       bp upstream of EcoRI
                                                                                                                                                                                                         RLYYRVMESMLKSEERLSIQNTSKLLHDNIFHMSLLACALEVVMATISRSISQNILG
GIDLSPWILLNVLHLAADDEEN EESE KARGNI KELEKE EEKE MESLANISD
SELEDLIKQKOREDTTHLISACDLHIFLAALDEELSVEKSTKKASI FUNIS
TANAFTQATSAFQTORELSSISLEENKYSITYKKHILLYEKLISERHELEH HU
EFQHILCNEYELMFDRHIDJIMMTSMYSITYKNILLKEELIVTAYKOLDHAVLEIEK
PVLIKFEFYDSIIVFYNSVEMAPEKTNILQYASTRPPTLSPIEHIPESTYKEPSSFLK
PVLIKFEFYDSIIVFYNSVEMAPEKTNILQYASTRPPTLSPIEHIPESTYKEPSSFLK
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TFIAPVDLDEMSETULSYPRTYETSVERFUNLLKEITETSTEVGVAMSELLKKTDVLFA
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/translation="MPPKIPFKTAATAAAAAABPPAPPPPPPPEEDPEGD8:FFEDERL
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/db_xref="GI:190959"
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/tissue_type="retina"
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                   98.9%;
99.7%;
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Patent, US 5912236-A 1 15 33N-1499;
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891 GAGACACAAGCAAGCTCAGCCTTGCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCA 195 	1 4d
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Sequence 2 from patent US $496731
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                                        1111 ATTCCTCCACACACTCCAGTTAGGACTGTTATGAAGAGTATGCCAAGAATTAATGATTGTTTTTU
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                                                                                                                                                                                                                                                                                                                                                                                                        871 AAAAATGTTTATTTCAAAAATTTTATACCTTTTATGAAIICI: 1166AC1161AACATCT
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                                                                                                                                                                              AAAGATCTAGATGCAAGATTATTTTTTGGATGATGATAAAAGTCTTGAGATGATTGTTATA 2511
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ATTGCTCGACACACTGCAGTTAGGACTGTTAFGAACACTATCCAACAATTAATGATGATT 2*91
                                                                                        GACAGITTTGAAACACAGAGAAAAACACAAAAAAAAAAGTAAACCTGATGAACAACACCTAATCTA
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Patent: US 5496731-A 2 05 MAR-1996;
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Xu,H.J., Hu,S.X. and Benedict,W.F.
Broad-spectrum tumor suppressor games, game products and methods
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2250 1311	2191 AARRATOTTCOTCATGCTGTTCAGGAGACATTCAGAGCGTCTTTTCATCAAACAACACGAG	qq Aç
2190 1371	2131 TATGGCATATGCAAAGTGAAGAATATAGAGCCTTAAATTCAAAATCATTGTAACAGCATAC } }	dd Yw
2130 1431	2071 CANAATSAGTATGAACTCATGAGAGAGAAGTATTGGAGGAAALIALGALGTGTTCAIG 	gd Áð
2070 1 49 1	2011 CLICIGICIGAGCACCCAGAATTAGAACATATCAGCGGGCCCTTTTTCCAGCACCGCCCCCCLLLLLLLLLL	Dp Dp
2010 1551	1951 CIGITITATAAAAAASIGITATOOGOTAGOOTATO TOOGGOTAAATAYAYITIGIGAACGO 	Qy Db
1950 1611	1891 GAGACAMAAMMAACTEAAMMTTEMAJAMMERAGAAAGMATEJAAALMAMMICTETTTMA 	qq Að
1890 1671	1831 CCTGTAAGATCTGCGAAGAAAAAAGGTTGCAGCTAGGGGTGTAAATTGTACTGGAAATGGA 	dd Yo
1830 1731	1771 GCTTGTCCTCTTAATCTTCCTCTCAGAAIAAICACACTGCAGCAGAIATGTATCTTCT LIHILIHHILIHHIHHHHHHHHHHHHHHHHHHHHHHHH	40
1770 1791	1711 TTATTTGATCTTATTAAACAATCAAAGGACGAGAAGGACCAACLGALCACCTTGAATCT	Оy
1710 1851	1651 CATTIAGAAGGAIGIGAACAICGAATCATGGAAIGCCTTGCATGGCTCICAGAFFCACCT	dq Db
1650 1911	1591 TACAAAGTGATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATAAAA LIIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Qy Db
1590 1971	1531 GGAAYAGATTTGTCTTTTCCCATGBAITCTGAATGTGCTTAATTTAAAAGCCTTTGATTTT	9ct Aō
1530 2031	1471 TGGGCTCTTGAGGTTGTAATGGGCACATATAGCAGAGGTACATCTGAGAATCTTGAGTTCT	ψy Db
1470 2091	1411 TOCATICAAAATITTAGCAAACTICTGAATGACAACATITTICATATGECTTTATTGGGG 	44
1410 2151,	1351 GRAGITEGGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAGAAGAACGACGATTA LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	gel ç
1350 2211	1291 AAATTIGCTAAADCTGTGGGAGAGAGAGGGGTCGTGGGAATTGGGATGAGAGGGATACAAACTT	441 V
1290 2271	1231 GTGAATCCAAAAGAAGTATACTGAAAAGAGTGAAGGATATAGGATACATCTTTAAAGAG 	₽ <i>§</i>
1230 2331	1171 ITAAATTCAGCAAGTGATCAACCTTCAGAAAATCTGATTTCCTATTTTAACAACTGCACA 123 	D Qy

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410 CALALAGGIGAIGHIGCICTIGTTTTAGTATTAGAATGGAATGGAATATATTGGAGGAGTAGAATTTAGAATAGAATTTAGAATAGAATTTAGAATAGAATTTAGAATTGAATGGAATTTAGAATTGAATGGAATTTAGAATTGAATGGAATTTAGAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAATTGAAAATTGAAATTTACCCTGAAAATTGAAATTTACCAATATTTACCAAAAATTGAAATTTACCAATATATTTACCAATATATTTACAAATATATTTACAAATATATTTACCAATATATTTACCAATATATTTACAAATATATTTACCAATATATTTACAAATATATTTACCAATATATTTACCAATATATATTTACAAATATATTTACAAATATATTTACAAATATATTTACAAATATATTTACAAATATATATATTTACAAATATATATTACAAATATATATATATATATATATATATATATATATATATAT	2911 PETIGINGATATAAAATGIGAAATGCAATTGTTTATAGGATHCCTAAGCACILOJ HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	2671 AACAHCTICCCAGGAGAGTICCAAA FETICAGCAGAAACTICGAGAAACAGCAGAAAACAACTICAGAAACAACTICAGAAAACAACTICAGAAAACAACAAAAAAAAAA	2431 CIGANGAGTCCATATANAATIICAGAAGGTCIGCCAACAACAACAACAAAAIGACICA HIIIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	2251 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAAAGAAAACAA
AAAA AAAA AAAA	AIG AAGI SAAGI	SA 24 CA 18 1A 25 1A 25 1B 26 C1 26 C1 95 C1 89	AIAII 2310 AIAII 1251 AIAII 1251 DAACC 2370 HHH DAACC 1151 TACCC 2430 TACCC 1131	

UY 422 ATACCAGCICCITCAGCAAACGAGCAGCAGCAGAACCTAAATTCTTAACTTACCAAACCAGACA 541 09 482 TEGCACCCCITCAGCAAAACGAACGAAACGAGAGCAGAACCTAAAATTGACAAAACCAAACCAGAACGAAACCAAAACGAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACGAAAACCAAAACCAAAACCAAAACCAAAACCAAAACCAAAA	QY 242 AGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGAAAAAGTAT AGAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAGAAAAAGAACTGT AGAAAAGTTTCATCTGTGGATGGAGTATTGGGAGGTTATATTCAAAAAAAA	UY 122 CGGACRACCICCIC ICGCICAGGCITGAGGTTGAAGAACAGAACCIGATTTTACTG 181 IHITHHILITHHILITHHILITHHILITHHILITHHILITHHILITHHILITHHILITHHILITHHILITHHILITH Ib 254 CGGACRACCTGCCTCTCGCTTCAGGCTTGAGTTTGAAGAAACAGAAGAACCTGATTTTACTG 3L3 UY 182 CATTATGTCAGAAATTAAAGATACCAGATCATGTCAGAGAGAG	QY 2. GREFFYATGOOGREYAAAAARTGOOGAAAAAAARGGOOGACGGOOGACGGOGGGGGGGGGGG	FASE COUNT 974 d 618 c 593 g 809 t ORIGIN OUGHY Match Hest Local Similarity 99.9%; Pred. No. 0; Maiches 2859; Conservative 0; Mismatches 2; Indels 0, Gaps 0;	n,b., lastom lastom loca l. ,	N. Sequence 3 from patent US 6074850. ARO98189.1 GI:12807446 ARO98189.1 GI:12807446 Unknown. Unknown. Unclassified.	DD 50 THICH CARCETATIOTH FAMALICAGGA HAFTCATAGT 7 RESULT 12 AKOUBLU9 AKOUB	* _ 4	OY 431 TGTTTFATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGGAAAGTATAACCATATGA 3450 	DB 230 AARTACTAATTITACACATTACATTIATTITATTITATTI
Oy 1442 176 1574 OY 1502 Db 1634 OY 1562	, , , , , , , , , , , , , , , , , , ,				Фу 902 Db 1034 Оу 962	0y 7 69 dd 99 dd 90 dd	Db 7 Q7 7 Db 8		9 du	9 del
FOR ACAGAMETER ANALOGIC LIARIES CON EL LISMON POLISMON PARAMETER ANALOGIC MANTALE LE PROPERTO DE LA CAMBANTE DE	TOGANATTURA CAGAGAGAAGAAGAATTATCCATTAAAATTTACCAAACTTCAAATCAAACGATTATCCATTAATCAAATTACCAAACTTCAAAATTACCAAAACTTCAAAATTACCAAAATTACCAAAATTACCAAAATTACCAAAATTACCAAAATTACCAAAATTACCAAAATTACCAATTACCAAAATTACCAATTACCAAAATTACCAATTACCAAAATTACCAATTACAAAATTACCAATTACCAAAATTACCAATTACAAAATTACCAATTACAAAATTACAAAATTACCAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAATTACAAAAAA	AICTGANT ICCIAIT ITTAACAACHGCACAGIGAAICCCAAAACAAAACAA IAICTGAAAACAACTGATITTAACAACTGAACAACTGAATCCCAAAACAAACAAAACA	ANASTAM CLISA ISANOSISSANTSIANTIC DECA, MACCA ACTA DELLA PARTECIA ACACA. HILLIHILLIHILLIHILLIHILLIHILLIHILLIHI	ANGGATAGGAAATTTATCTTAAAAATAAAGATCTAGATGCAAGATTATTTTTTGGATGAAAGATCTAGATGCAAGAAAATTATTTTTTGGATGAAAGATGAAAACTACTGTTGGAAGTGCAGAGAGAG		782 GGAGTGCANGGATAGNAAACAAGTAGAAAATGATATAGAAATTATTGAANTTATTGAANTATATATA	794 TGCTATGTGCCTGACTATTTATTAAACTCTCACCTCCACTTCAACTATTCAAACAAC	TATTAGCIAAAGGGGAAGIATIACAAAIGGAAGAIGAICHGAILIGAILIGAGIIAAAIIAAAIGGAAGAIGAICHGAILIGAILIGAGIIAAAIIAAAIIAAAIIAGAAIAGAIGAAGAIGAILIGAILIGAGIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAIIAAAA	542 GTTCGATATCTACTGAAATAAATTCTGCATTGBJGCTAAAAGHICLIGGALCACATTTT GG 	614 TUDGAGUGUHGAGAAALIGHALALITITITITITITITITITITITITITITITITITIT

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DOUGLAS ANTELMAN, RICHARD IT GREGORY, KENNETH N WILLS

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Hest Local Similarity 99.9%; Fred. No. 0;
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Antolman, E., Gregory, E.J. and Wills, K.
Rethnoblastoma fusion proteins
Patent, US 6379527 A 3 30 AFE 2002;
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Tissue specific expression of retinoblastoma prote.
Patent: JP 2001503638-A 2 21-MAR 2001;
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Lee,W.H., Shew,J.Y., Hong,E.D., Sery,T.W., Donoso,L.A., Young,L.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia: Outhoria: Primates; Catarrhini; Hominidae; Homo.
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781 TCATTTCAGTTAATGCTATGTGTCCLTGACTALLTTALTAAACTCLCAGCTGCATGTTG 840
                                                                         182 SerFheSIntæiMetizæfysValtæiAsplyrPheTfetystæiSerFroProMetizæi 201
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TAKALTQATSAFQ (QBELKS ISLST) NKVYKTATI KTNIDJEKLISEHPELEHTIMI
LEQHTIQNEYFI MEDHHIDQIMMISMYSTIVKNITA KEKTI VIAYADI HAVQETEK
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441 1560	422 ArgValMetCluSerMetLeulysSerCluSlbSlbArgLeuSerlleGlnAshPheSer 	dd Yo
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341 1260	322 ArgTheFloArgLysSmlAsuLo.A.y&luGluValAsuValIleFloFloHisTheFlo 	95 \$
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Location/Qualifiers
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Harrigan,S., Sappet,D.R. and Weaver,E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
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Partial inactivation of the RP product in a family with incomplete
penetrance of lamilial relinoblastoma and benign relinal tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 813-5868
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SPLFDLIKQSKDREGPTDH.ESAGPI.NLPLQNNHTAAAMYL.GFMSSFKKKGGTEMBE
TANAETQATSAFQIQKMI.KSTSLSLFYKKVYRLAYLRI.NTLJEKLI.SEHPELLEHTIWI
                     premature stop"
                                                                                                                                                                                                                                                                    premature stop"
/replace-"ca"
518. .637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /replace="t"
275, .401
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/citation-[5]
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RVLKESAEGSNPEKELKKLEET TETSPEAGGSKEILPTESKEGGALAEMISTKTOMV.NSI
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LCKEHECNTDEVKNVYFKNFTPFMNSLCI.VTSNGLFEVENLSERYEETYLENKT.TJAR
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/protein_id="AAB59465.1"
/db_xref="G1:793995"
                                                    /note="Tumor COS561 unilateral frameshift matation
                                                                                       /gene="RB1"
                                                                                                                                                          /number-4
                                                                                                                                                                                          /note-"G00-118-734"
                                                                                                                                                                                                                          /qene-"RB1"
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                                                                                                                                                                                                                                                                                                                                                                                               /qene-"RB1"
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IFTAAVDLDEMSFTETELQKYTETSVHKFFNLLKETETSTKVCSAMSFLLKKYLVLFA
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|452| |1475
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1077. .118
/note-"G00:118-234"
                                                                                                       Troplane man
                                                                                                                                       resulting in premature stop: Associated with this mutation is a large 1994.3 sub-band deletion: G00-118-734  
/eilation [5]
                                                                                                                                                                                                                                                   /note-"lumer desil quilateral trameshitt mutation
                                                                                                                                                                                                                                                                                                       /qene "RBI"
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1187. .1264
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stop: G00 118 734"
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/dene-"RBI"
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                           /qene-"RHI"
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                                                GluLeuGluHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeu 661
                                                                                              LysLysClySerThrThrArqValAsnSerThrAlaAsnAlaCluThrClnAlaThrSer 601
                                                                                                                                                                                                                                                                                               CATCGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAA
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                                GAATTAGAACATAICATCITAGAAAAAATTACAAGAACACCCTGCAGAAATAAATTAAACTC 2219
                                                                                                                                                                                                                                                                                                                            ProLeuGluAsuAsuHisThrAlaAlaAspMetTyrLeuSerFroValArgSerFroLys 581
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DryJa,T.F. and Friend,S.
Human DNA in the diagnosis of retinoblastoma
Patent: MP 0254031-A2 1 04-MAP-14AR.
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               62 LysLysGluLeuTrpClyTleCysTlePheTleAlaAlaValAspLeuAspNluMetSer
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             ANTISENSE RNA EXPRESSING VECTOR
PATENT: JP 1947023844-A 1 28-TAN-1947.
CHIKYU KANKYO SANSYO SIJUTSU KENKYU KIKO
OS Mus musculus (nouse)
PN JP 1947023884-A/1
                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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PF KOBAYASHI MASAYUKI, YAMAHCHI YHKIKA, IANAKA AKIK ES CILDNIS PO (ANTROLOGO ARTHABAR A GILDNIS PO (ANTROLOGO ARTHABAR A GILDNIS) A TIESICHARA)
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342 1203	ValargThrValMetAsnfhrileGluGlniceuMetMettleLeuAsnScralaScrasp 3 	ы
362 1263	GloproserdloasoleotleserTyrPheasolasoCysThrValAsoProLysGloSer 38	2
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102	Glydhodlydystaldhollodlysordharatyrlystoadlyvalaratoafyrtyr 42 	K.
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462 1563	Met ALa thi Tyr Set Ar gSerThrSerGluAsni.euAspSerGlyThrAspl.euSerPhe 48 	C
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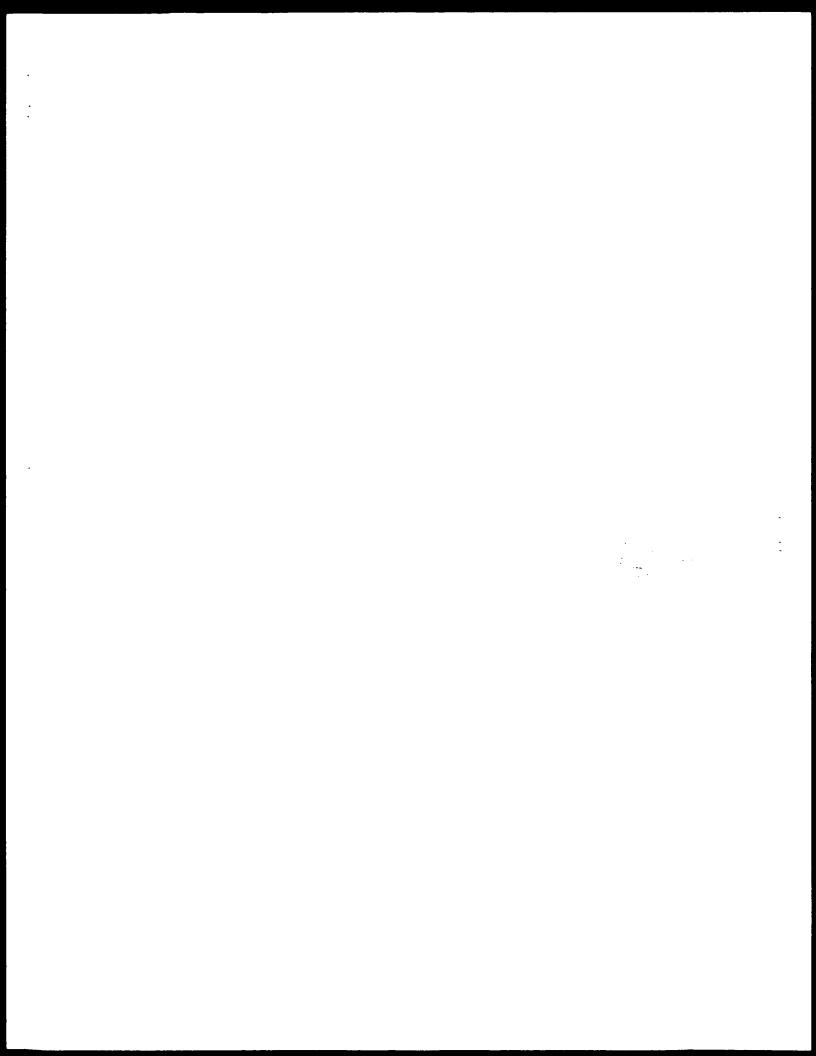
Oy 882 LysMetAshAspSerMetAspThrSe ::: :: 	Oy 862 SerLysPheGlnGlnLysLeuAlad! IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 842 LegArgPheAspilediuGlySerAs H+H+H+H+H+H+H+H+H+H+H+H+H+H+H+H+H+H+H+	Gy 822 ScrasparqValleulysarqSeraladir 	2 FleGlyGluSerPheGlyThrSere 		Oy 752 SerProtouArd Hebrochydlyd 	742 ArgProProThrLeuSerPro1 	Oy 722 PhoTyrAssSerValPhoMorGluArgLouf yet 11	Oy 702 ValGingfuthr PhetysArgVallaru [[]][][][][][][][][][][][][][][][][][]	Oy 682 tysasnileaspleutysbhetysti 	2 MetArqAspArqHisLeuAspGlu 	Oy 642 GluteugluHis HerleTrpTbrte HILLHILLHILLHILLHILLHILLHILL Db 2100 GAGCTAGAGCACATCATCTGGACTCT	0y 622 TyrarqLesalatyrLesarqLesasathrLesey 	Uy 602 AlaPheGloThrGloLysProLeuLys 	82 LysLysGlySerThrThrArgVa :::	-62 ProteuGthAshAshHistbrAl
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Command line parameters:

MODEL-frame:_p2n.model -DEV-x1h

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MODEL-frame:_p187-p2n.model -DEV-x1h

-Q-x2n2_p187-p2n.model -DEV-x1h

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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                                                                                        ATATCTACTGAAATAAATTCTGCATTGGTGGTAAAAGTTTCTTGGATCACATTTTTATTA 738
Retinoblastoma fusion proteins
Patent: US 6379/Q7 A 3 30 APR 2002;
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RESULT 4
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Antelman, B., Gregory, R.J. and Wills, K.N.
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381 ThrfleGInGinLeuMetMetfleLeuAsnSerAlaSerAspGinProSerGDAstLeu
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2.459 CGTGTTTTGATCAAAGAAGAAGAGGAGTATCTATTATAGTATTCTATTAAGTCGGTCTTC
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US-09-026-459A-51 (1-928) x HUMRHSA (1-2994)

Query Match:

Best Local Similarity: Percent Similarity:

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1 (bases ! to 2994)
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360	LysThrLouGlnThrAspSerl!eAspSerPheGluThrGlnArgT	341	ОУ
1218		1159	
340	TyröluöluIleTyrLeuLysAsnLysAspLeuAspAlaArqLeuPheLeuAspHisAs	321	B &
1158		1099	
320	AsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSer	301	B 8
1098		1039	
300	HischucysasnileaspCluvailysasnvaityrPhctysasnPhellePtoPheMet	281	ψy
1938		979	
280	AlaArqIleAlaLysSlnLeuSluAsnAspThrArqIleIleGlsValLeuCysLysGlu	261	₽ 3
978		919	
260	ThrâlaVallîeProileAssGlySerProArqThrProArqArqGlyGlnAsnArqSer	241	₽ %
918		859	
240	**TysValle_As;**Y:Pheilei;steuSetPtoPtoMetLeubsCluPtoTytLys	221	Db 13
858		799	
220	AlaLysGlyGluValLeuGlmMetGluAspAspLeuVallIeSerPheGlnLeuMetLeu	201	9d
798		739	48
200	IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu	181	9dd
738		679	8A
~ 8	LeuPheSerLysLeuGluArgThrCysGluLeuHeTyrLeuThrGlnProSerSerSer 	161	Dp QA
160	SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla	141	Dþ
618		559	
140	ClnLysAsnIleGluIleSerValHisLysPhePheAsnLeuLeuLysGluIleAspThr	121	94
558		499	
120	PROPERTY OF THE PROPERTY OF TH	101 439	941 A.A.
199	ValSerSerValAspGlyValLeuclyGlyTyrTleGlntystystysGlsLeuTrpGly	81	dd
438		379	YY
80	CysGlnLysLeuLysIleProAspHisValArqGluArqAlaTrpLeuThrTrpGluLys	61	44
378		319	
60	AspicuProLeuValArgLeuGluPheGluGluThrGluGluProAspPheThrAlaLeu	41	pp
318		259	7
40	ProAlaProProProProProProProProAluGluAspProGluclaAspSexGlyProGlu	21	qq
258		199	
20	1 MetProProLysThrProArgLysThrAlaAlaThrAlaAlaAlaAlaAlaAlaGluPro 2	1	qa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinoblastoma protein.
Homo sapiens (clone: p4.7R) cDNA to mRNA.
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Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 CAGAAAAACATAGAAATCAGTGTGCATAAATTGTTTAACTTAGTAAAAGAAATTGATAGG
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VKLEFEEFEEFDFTALCOKLK FEDHVKERAWI IMERVSSVETVIJJEV JOKKKELWEIF
IFTAAVDLDFMSFTETETGKNIFTSVHKEFFNITKFITTSTKVDNAMSFLLKKYDVLFA
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/db_xre1="GI:190946"
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/eodon_start=1
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l AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 56	1 LouAsnLouLysalapheAsppheTyrLysVallleGluSerpheTleLysalaGluGly 5 	01 SerThrSerGInAsnLeuAspSerGlyThrAspLeuSerPheProTrp11eLeuasnVal 5 	IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThrTyrSerArq 50 	uSerfleginasn?heSeriystæulcuAsnAspAsn 4 		AspiledlytyrilephetysdlutysPheAlatysAlaValSlydlsGlydysValGlu 4	01 HeSerTyrPbcAshAshCysTbrValAshProLysGluSerTleLcuLysArgValLys 1 	12 4	361 AsnLeuAspGluGluValAsnValILeProProHisThrProValArgThrValMetAsn 380 	341 LysThrLeuGlnfhrAspSerileAspSerPheGluThrGlnArgThrProArgLysSer 360 	321 FyrGluGluHefyrLouLysAsmLysAspLeuAspAlaArgLouPheLouAspHisAsp 340 	1 AshSerLeuSlyLeuValThrSerAshSlyLeuProGluValGluAshLeuSorLysArg 32 	281 HisGluCysAsnileAspGluVallysAsnValTyrPhelysAsnPhetleProPheMet 300 	61 Albargilealbhyscini.eucluAsnaspfhrargileileciuvail.cucyslysciu 28 	gGlyGlnAsnArgSer 2 αGTCAGAACAGGAGT 7	221 CysValleAspfyrPheflelysLeuGetPtuPtuPtuMetLeufeufysGiuFtuTytlys 240 	201 AlalysülyülüvalleudleMaspAsple.VailleSetFheSitLeumettee 220 	181 IleSerThrGluIleAsnSerAlaLeuValLeuLysValSerTrpTleThrPheLeuLou 200
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27.73	ACCCTGCAGAATGAGTATGAACTCATGAGAGACACC	7	Dβ
7	TpThrLeuEheGloHisThrLeuGluAsuGluTyrGluLeuMetArqAspArqHisLeu	9	Qy
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580	LeualaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspAruglu		оу
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56	AsnicuThrargGluMctIleLysHisLcuGluArgCysGluHisArgileMctGluSer	541	Oy
1817		1758	dd
1.4°	LeuAsnLeuLysAlaPheAspPheTyrLysVallIleGluSerPheHeLysAlaslaslasl		4d
1757			4d
16.95	SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpILeLeuAsnVal 		9 8 8 VQ
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1	LeuLysSerGluGluGluArqLeuSerIleGlnAsnPheSerLysLeuLeuAsuAspAsn 	i 6	Qy Db
450	TleGlySerGlnArgTyrLysLouGlyValArgLouTyrTyrArgValMetGluserMet		Qy
1517			Oy
440	Asp:leClyTyrilePhelysClulysPheAlalysAlaValClyClnClyCysValGlu	421	Dh
1457		1398	Qy
420	IleSerTyrFheAsnAsnCysThrValAsnFroLysSlaSerIleLeuLysAraValLys	401	Q;
1397		1338	Db
1245	ThrileGinGinLeuMetMetIleLeuAsnSerAlaSerAspGinProSerGiuAsuLeu 	381 1278	Ωγ
380	AsnieuAspGluGluvaiAsnvallieproproHisthtprovaiAtqIhtvai	361	Qy
1277		1218	db
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Draft entry and computer-readable copy of sequence in [1] kindiy provided by P.Mookstein, 27-APR 1987.
                                                           Froc. Nat
88320373
                                                                                                                                                      2 (bases 1 to 480) Lee,E.Y., Booksteld,R., Young,I. T., Tin,C. T., Posenteld,M.S.
                                                                                                                 Molecular mechanism of retinoblastoma gene inactivation
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                                                                                                                                                                                                                                                            and sequence
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Human retinoblastoma susceptibility gene: cloning, identification.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Momo sapiens (clope: FB-[1,5])
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                                                                                         GTTTCATCTGTGGATGGAGTATTUGGAGGTTATATTCAAAAGAAAAAAAAGAACTGTGGGGA 438
                                                                                                                 Val Sex Sex Val Aspel (yVal Lead Lyd) yli yli (cC) ni ysi ysi ysi ysi fisculfapid yli 100
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ATCTCLATCLLLATIGCACGAGITIGACCTAGATGAGATGTCGTTCAC-TILACTGAGCTA 497
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LFGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESEGTSEKFQKINQMVCNSD
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SPLFDLTKQSKDREGPTDHLESACPLNLPLQNNHTAADMYLSPVRSPKKKGSTTRVNS
TANAETQATSAFQTQKFLKSTSLSLFYKKVYRLAYLRINTLCERLLSEHPELEHTIWT
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SUQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGGVEIGSQPYKLGV
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VRLEFFFTFPPDFTALCQKLKTPDHVPEPAWLIWEKVSSVIMMVL/GGYTQKKKELWGTG
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                                      242 GGAGTATTGGGAGGTTATATTGAAAAGAAAAAGCAACTGTGGGGGAATGTGTATGTTATT
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Fung, Y.K.T., T'Ang, A., Murphree, L.A. and Benedict, W.F.
A method for detecting the predipposition to retinablastoma and a method for detecting the predipposition to retinablastoma and a retinoblastoma gene in tumors using a retinoblastoma gene in tumors using a
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                                                                                                                            341 LysThrLeu6InThrAspSerlleAspSerPheGlnThrGlnArq1hrProArqLysSer 360
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SUMMARIES

44 207 6.1 480 9 HUMRBSY79	43 218.8	220.8 6.5 36.03 6	41 220.8 6.5 3499 f.	40 220.8 6.5 1698 6	39 220.8 6.5 901 6	225.2 6.6 110188 2 7	248 7.3 301 11 673442	248 7.3 301 9	288.6 8.5 944 5	347.2 16.2 426 9 A	483.2 14.2 2102 10	539.2 18.8 2730 5	718.6 21.2 1386 5 A	723.4 21.4 [8]5]]	835 24.6 180388 9	8 835 24.6 62825 9	7 835 14.5 2952 9	835 34.5 2352 5	1052.8 31.9 2898 5	1394 41.1 1554 4	1472 43,4 4541 5	43.7 3456 S U	2328.6 68.6 4432 10	2338.2 68.9 4591 10	2339.8 69.0 4591 6	2686.4 79.2 2995 6	79.3 2994 9	269) 79.3 2944 6	15 Oct 7 1 100	79.3 2994 5	2691 79.3 2994 6	3222.4 95.6 9292 6	3222.4 95.0 4242 6	2.4 95.0 K232 K	95.00 3232 6	3322.8 98.0 4580	98.7 4740 9	81,4 99,7 4597 6	99.7 4597 6	99.7 4839 9	3 99.7 4839 6 /	1 3383 99.7 4600 9 HUMKBALKA	Score	Result Query
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11111	AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	SUNCI	RESULT 1 HUMRHALRA
Difference of a DNA Sequence in retinoblastomas and mescachymas	Friend, S.H., Horowitz, J.M., Gerber, M.R., Wand, X.F., Petermann, E.	Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 10 4600)	Homo sapiens Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Difeleostemi:	Homo sapiens (clone: p4.7k) cDNA to mkNA.	retinoblastoma protein.	M33647.1 GI:190945	M33647_J02994	Human retinoblastoma associated (kBl) mRNA, complete eds.	HUMRHATRA 4600 bp mena linear for 12 JUL 1995	

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2649	2590 ATGAATGATAGCATGGATACCTCAAACAAGGAAGGAAGAATGAGGATCTCAGGACCTTGGT :	Š
2748	2689 AAATITCAGCAGAAACTGGCAGAAATGACTTCIACTGGAACAGGAAIGCAAAAGCAGAAA	ē
2589	2530 AAATTICACCACAAACTOCCACAAATCACTICTACTICTACTCCAACACCAAAAGCAGAAA	Ş
2688	CONTETEGATATEGAAGATYAAATGAAGAYAAATGGAAAGTAAAYATTCTCCCAAGGAGAGGTCC	12b
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2469	GACCETGTGCTCAAAAGAAGTGCTGAAAGGAAGGAAGCCTCCTAAAGCACTGAAAAAACTA	çy
2409 2568	GOTGAATCATTCGGGACTTCTGAGAAAGTTCCAGAAAATAAAT	Ē Š
2349 2508	TCAGAAGGTCTGCCAACACAACAAAATGACTCCAAGATCAAGAATCTTAGTATCAATT	물 것
2289, 2448	CCCTTACGGATTCCTGGAGGGAACATCTATATTCACCCCTGAAGAGTCCATATAAAATT	95 63
2229 2388	COORT PARTY OF CARCACIACY PARTAL FOR FOR AGORDETIC ACAGOT FIGURACITE CACACITE CACACITE COORT CACACITE CACACITE COORT CACACITE CAC	ş 3
2169 2328	TATAACH GABROTECARGA AGAGACH GAAAACAAA FETT FGCAGTATGCTECAGCAGG - - - - - - - - - - - - - - - - - -	돌왕
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2049 2208	AATATAGAYYTTAAAYTYAAAATYATTGTAACAGYATAYAAGGATCTTYCCCCATGCCGTT -	F &
1989 2148	AGAGAGAGA PETGGAACCAAAPTA IGA I GI FECCATGI A I GGCATATOCAAAGTGAAG 	£ &
1929 2088	TTAGAAN'ATATPATETBGAPPETTTTCCAGRACACCCTGPAGAATGAGTATGAACTCATG 1111-1111-1111-1111-1111-1111-1111-11	<u> </u>
1869 2028	1810 - CODT FACOCHA POTECCOCCHANA FACACHT LO TONACCOC FECTIC TOTTC TOTTC ACCACCACAGA - 1 	<u>\$</u> \$
1809 1968	1750 TECYAGACYCAGAAGCCAFFGAAALCTACYTCTCTTTTCACTGTTTTATAAAAAAGTGTAT 1 	F G
1749 1908	1690 AAARSTICAACTACGGGTGTAAATTCTACTGCAAATGCAGAACACACAC	<u> </u>
1689	1630 - CICCAGAATAATKATKACIGKAGCAGATAIGIAIGIKTETEKECIGIGKAGAGATGTECAAAGAAA I 	15 GA
1629 1788	1570 FCAAAGAACGACCAAACGAACAACTGATCACCTGAARG GCCTGGTGCCCCTTAATCTTCCT 1 	£ &
1569 1728	1510 CGAATCATGGAATCCCTTGCATGGCTCTCAGATTCACCTTTATTTGATCTTATTAAACAA 156 	<u> </u>

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Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapoutic screening using signature
Patent:
                                            gene sets
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                  6 (sites)
Kratzke,R.A.,
                                                                                                        with bilateral and unilateral retinoblastoma
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7451
                                                                                                                                                  Hogg, A., Hia, B., Gnadim, 2. and Cowell, J.K.
Molecular mechanisms of oncogenic mutations in tumors from patients
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Cowell,J.K.
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Br. J. Cancer 68 (5), 958-964 (1993)
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Proc. Natl. Acad. Sci. U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapieus
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                                                                                                                                                                                                                         8217609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens cDNA to mkNA
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in therson, G.A., Hogq, A., Coxon, A.B., Geradts, J.,
and Kaye, F.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E-mail: brenda@hafiz.eric.on.ca
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IE IAANDLDEMSETETELCKKNIE EISVIIKFFNILKE I OTSTKYUNAMSPILKKYDVLEN
LESKLERTGELIYLIQESSISTETINSALVLKSWITELAKGEVLQMEDDLVISFQL
MICVLDYFIK IS.SEPMLLKEPYKIAV I D'INGSDETPRROONSSAKIAKOLDENDEK ILFQL
CKEHECNIDEVKNVYFKNEI PEMNSIGIVESNGIPEVENISKRYEE I YLKNKDIDAH
LEIDHDKILGIDS I DSEFIDKTEKKSNLDEEVWYI PPH IPVRIVMNTI QOLMILNSA
SDQPSENLISFYNNGTUPKKESILKERWYDTGY YEFKFRAKAVGGEVELIGSLGYKLGS
RLYFRVMESMLKSEEERLSIQNESKLLNDNIEHMSLLACALEVVMATYSRSTSQNILDS
GTDLSFPWITINVI NI KAFDEYYVIESETKAEGNICHTERMIKHLEPGEIDFIMESLAWLSG
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IPGGNIYISPIKSPYKTSFGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
FVLKESAEGSNPPKPLKKLPFDIFGSDEAFGSKHLPGESKFQQKLAEMTSTPTPMQKQ
                         /number-4
537. .542
                                                                                                                                                                                                                                               /number-3
506. .509
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Zeitation [5]
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                                                                       /note="G00:118-734"
                                                                                                                                           /replace-"ca"
                                                                                                                                                                  /mote="PBFF4 bilateral familial deletion mutation causing
promature stop"
                                                                                                                                                                                                                     /qene-"RB1"
                                                                                                                                                                                                                                                                                               /noto="G00-118-734"
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TANAETQATSAFOTOKPTKSTSI SLEYKKVYFLAVLENTIJCEBILLSEHPELEHTIWI
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/preduct "relicablastor= cospectibility protein"
/protein_id="AAB59465.1"
/db xref="d1:794995"
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/map="13q14.2"
1. .4839
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/.ouc-"Tumor GOS563 unilatoral mutation cassing promarcie
stop: GO0-118-734"
/citalio-[5]
/replace-[1"
                                                                                                       /citation-[5]
/replace-"t"
1352. .1375
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/citation-[5]
/replace="ta"
621..622
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856. .998
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                  resulting in premature stop: Associated with this mutation is a large 13q14.3 sub-band deletion; Go- 118-734" /citation=[5]
                                                                                                                                                         /note-"Tumor GOS559 mutation causing premature stap 600\,{}^{\circ}118\,{}^{\circ}734\,{}^{\circ}
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1265. .1352
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/replace-"ca"
                                                                 /note-"Tumor GOS13 unilateral trameshift matation
                                                                                      /gene-"RB1"
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745. .855
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ANTOTTTO TAAN GATAGGANAAAATTTATCTTAAAAATAAAGATGTAGATGGAAGATTA HHHHHHHHHH	GHCICIGIAAAGACAIGAAIGIAAIAIAGAGGGGAAAAAIGITTATTTCAAAAAT HHILLHILLHILHHILHHILHHILHHILHHILHHILHHI	AAAGAACCATATAAAACAGCTGTTATACCCCATTAATGGTTCACCTGGAACAGCCAGGGGA HHHHHHHHHHHHHHHHHHHHHHHH	ATCACATTTTATTAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTCA LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	GARGRAFIGITITICACTOTORCAGCAAATTGGAAAGGACATIJIGAACTTATATATTTTTGACA [11] [1] [1] [1] [1] [1] [1] [1] [1] [1	ACTITIACTICAGCITA/AGANAK/ATAGANAK/CAGTGGTCCATAAATOTTTA/CTCTA 	THANCITUS AND AND TETEVATORS IS SATORANGED TO SAGOTATATIVE CANADAMA AND AND AND AND AND AND AND AND AND AN	GATTTTACTGGATTATGTCAGAAATTAAAGTATGGGAGGTCATGTCAGAGAGAG	99.7%; 100.0%;	[1854
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MAGATETAGATGOA 	MAAATGITTATTICA HHHHHHHHAAAATGITTATTTCA MAGACTTCCAGAGG HHHHHHHHHHHHHHHHAAGGACTGCAGAGG	CACCICGAACACCA	AAGATGATCTGGTGA	TGGAACTTATATAT LIHHHHHHHHH UTGAACTTATATATT TGGTGCTAAAAGTTT LIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	ATAAATTGTTTAACT ATAAATTGTTTAACA ATAAATTGTTTAAGA CAAGACTGTTGAAGA	GAGGTTATATTCAAA GAGGTTATATTCAAA AACCTAGATGAGATG	ATGTCAGAGAGAGAG - - - - - - - - - ATGTCAGAGAGAGAG	9; Length 4839; 0; Indels 0	
GATTA 849	AAAAT 729 AAAAT 1022 TTGAA 789 	GGCGA 609 CGCGA 902 TTGAA 669 	TTTCA 489	TGACA 369 11111 TGACA 662 CTTGG 429 11111 CTTGC 722	TACTA 249	AGAAA 422 AGGTTC 189 	CTTGG 69 C TGG 362	0; Gaps 0;	
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3130 CTCTTCTGCAAAAATGGATATTAITAGAAATTAGAAAAAAATTACTAAITTTACACAT1A 3189
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Dryja,T.P. and Friend,S.
Human DNA in the diagnosis of retinoblastoma
Patent: FP 0259031-A2 1 09-MAR 1988;
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1329 1485	1270 CTPTBAA GACAACATTI LCATATGICTITAT GGCGGGCGCTCTGAGGTTGTAATG LLLLIH HILLIH H	DP 1
1269 1425	1210 GTAATGGAATCCATGCTTAAATCAGAAGAAGAACGATTATGCATTGAAAATTTTAGCAAA 	D# 1
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1149 1305	1090 CIGAAAAFAGIGAAGGATATAFGATAGATACATCITTAAAGAGAAATTIGCTAAAGCIGTGGGA 	94
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Humann retinoblastoma susceptibility mRNA, complete eds.
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rec Mail Acad. Sci [I S A 85 (16), 6817-6821 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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STARWMESMLKSELEKS QOMPSKLINDNIPHENSLIACALHVVMATYSETSSOLDS
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1143 ATTTTTGGATGATGATAAAACTCTTCAGACTGATTCTATAGACAGTTTTTGAAACAGAG

1988 2282	1929 GAGAGACAGGCATTTGGACCAATT 	P 99
1928 2222	1869 ATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGC	£ &
1868 2162	1809 TCGGCTAGCCTAFCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTGTGTGAGCACCCAG 	45 45
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1748 2042	/ 1689 AAAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACCAAGCAA 	43 43 43
œ 8	/ 1629 TCTCCMAAATAATCACACTGCAGCAGATATGTATCTTTTCTCCTGTAAGATCTCCAAAGAA 	961 VA
52	/ 1569 AFFAAAGGACGAAAGGACGAACTGATCAGCTTGAATCTGCTTTGFCCTCTTAATCTTCC FILLILITITITITITITITITITITITITITITITITIT	40
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1448 1742	/ 1389 ATGGATTCTGAATGTGCTTAATTTAAAAGGCTTTGATTTTTAGAAAGTGATGGAAGTTT	45 An
ີ ອີ ອີ	/ 1329 GGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCTGGAACAGATTTGTCTTTCCC 	46
NO NO	/ 1269 ACTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCGTTGCTCTTGAGGTTGTAAT 	94 64
1268 1562	7 1209 AGTAATGGAAFCCATGCTTAAATCAGAAGAAGAAGATTATGGATTGAAAATTTTAGGAA 	4d 50
0 0	/ 1149 AVAGGSTEGTGGGAAATTGGATGAAGGGATACAAAGTTGGAGGTTGGATTGTATTAGGG 	441 451
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1382	/ 1029 ACCITCAGAAAAFCIGATI ECCIA ETTAACAACIGCACAGIGAAFCCAAAAGAAAGTAT 	£ &
1028 1322	/ 969 TAGGACTGTTATGAACACTATCCAACAATTAATGATGATGTTTAAATTCAGCAAGTGATCA	4d 45
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                                                                 250 AAAGAAATIGATACCAGTACCAAAGTIGATAATGCTATGTCAAGACTGTTGAAGAAGTAT 309
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Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Renedict,W.E.
A method for detecting the predisposition to relinoblastoma and
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                                                                   ATTCCTCCACACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATTT 846
                                                                                                                                                    GACASTTTTGAAAFAFAGAGAAFAACASAAAAASTAACCTTGATGAAGAAGGTGAATGTA
                                                                                                                                                                                                                                            AMAGATOTAGATGOAAGATTATTTTTGGATOATGATAAAAOTOTTTOAGAOTGATTCTATA
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                                                                                                              ATTCCTCFACACACTCCAGITAGGACTGITATGAACACTATCCAACAATTAATGATGATT 1008
                                                                                                                                                                                                                                                                                   AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATA 888
                                                                                                                                                                                                                                                                                                                                                                        NATGGACTTCCAGAGGGTFGAAAATCIIICIAAACGAIACGAAGAAAIGTAGGTTAAAAAT 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAAATGIITATTTCAAAAATTTTAIACCTTTTATGAATTCTCTTGGACTTGTAACATCT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG
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    AATGGACTTCCAGAGGTTCAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT 666
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Xu,H.-J., Hu,S.-X. and Benedict,W.F.
Broad-spectrum tumor suppressor genes gene products and methods for
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                                      649 AATGATACAAGAATTATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 708
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AR072032
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Patent: US 5912236 A 2 15 JUN-1899;
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1488 1911	429 FACAAAGIGAICGAAAGTTEFATCAAAGCAGAAGGCAACTEGACAAGAGAAATGATAAAA 	Οy
4.2 97	369 GGAACAGATTTGTCTFTCCCATGGATTCTCAATGTGCTTAATTTAAAACCCTTTGATTTT 	9t1 VQ
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                                                            1207 GGAACAGAFITGTCTTTTCCCATGGATGTGATTTAAAAFTTTAAAAGCCTTTTGATTTTT
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                                                                                                                        1369 GGAACAGATTTGTCTTTCCCATGGATTCTGAATGTGCTTAATTTTAAAAGCCTTTGATTTT 1428
                                                                                                                                                                                                                                          1309 TOCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT 1368
                                                                                                                                                                                                                                                                                                       1987 TCCATTCAAAATTTTAGCAAAGTTCTGAATGACAACATTTTTCATATGTCTTTATTGGCC 1146
                                                                                                                                                                                                                                                                                                                                                                                                                            1027 GGAGTTCGCTTGTATLACCGAGTAALGGAALCGATGCTTAAALCAGAAGAAGAAGAACTALLOHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1189 GGAGTTCGCTTGTATTACCGAGTAATGGAATCCATGCTTAAATCAGAAGAAGAAGAACATTA 124F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1129 AAATTTGCTAAAAGTGTGGGAGAGGGTTGTGTGGAAATTGGATGACAGGGATAGAAAGTT 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1069 GTGAATCCAAAAGAAAGTATACTGAAAAAGAGTGAAGGATATAGGATAGATGTITIAAAGAG 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              967 AAATTTGCTAAAGCT3TGGGACAGGGTTGTGTCGAAATTGGATCACAGCGATACAAACTT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 GTGAATGCAAAAGAAAGTATACTGAAAAGAGTGAAGGATATAGGATACATGTTTAAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 TTAAAFIGAGGAAGTGATGAAGCTTGAGAAAATGTGATTTGCTATTTTAAGAAGTGCAGA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            787 ATTCCTCCACACTCCAGTTAGGACTGTTATGAACACTATCCAACAATTAATGATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           949 ATTICCTICCACACACICCAGTTAGGACIGITATGAACACIAICCAACAATTAATGATT 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 GACAGTITLICAAACACAGAGAACACCACGAAAAAGTAACCTIGATGAAGAGGTGAAIGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          889 GACAGITITGAAACACAGAGAACACACACAAAAAAAGIAACCIIGAIGAAGAGGIGAATGIA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   829 AAAGATCTAGATGCAAGATTATTTTTGGATCATGATAAAACTCTTCAGACTGATTCTATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              769 AATGGACIICCAGAGGTTGAAAATCTTTCTAAAGGATACGAAGAAATTIAICTIAAAAAAI 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 TICACCTICGAACACCCAGGCGAGGTICAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 TTGGTGCTAAAAG11TCT1GGA1CACA111111ATTAGC1AAAGGGGAAAG1A11ACAAA1G 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACCTCGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAACAACTAGAA
                                                                                                                                                                                 {\tt TGCGCTCTTGAGGTTGTAATGGCCACATATAGCAGAAGTACATCTCAGAATCTTGATTCT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAATGTTTATTCAAAAATTTTATACCITTATGAATICTCTTGGACTTGTAACATGT 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANAANTGITTATITCANAANTTITATACCIIIIAIGAN ICICIIGGACIIGIAN AICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGATGATCTGGTGATTTCATTTCAGTTAATGCTATCTGTCCTTGAGTATTTTATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGGACTTCCAGAGGTTGAAAATCLLLCTAAACGALACGAAGAAATTTATCTTAAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGATACAAGAATTATTGAAGTTC1C1G1AAAGAACA1GAATG1AATATAAGATGAGGTG-546
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                                ANACATOTUCCAGGAGAGTCCAAATTTCAGGAGAAACTGGCAGAAATGACTTCTACTCGA 2568
                                                                                          CTAAACCACTGAAAAACTACGGTTTGATATTGAAGATATGAAGGAATGAAGGAGAGGAATGGAAGT 2346
                                                                                                                                                                                                                 CONTACAACHIIITOOTIAGITTOACCONIITAGGGATTCCTGGAGGGAACATCTATATIITICACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTEGATTOTATTATAGIATICIATAACIOGGICIICAIGCAGAGACIGAAAAAAAAAAAAATATT 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAATGAGTATGAACTCATGAGAGAGAGAGGGATTTGGACGAATTATGATGATGTGTGCCATG 1968
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                                                                                                                                                    CCTANACCACTGANANACTACGCTTTGATATTGANGGATCAGATGANGCAGATGGANGT 2508
                                                                                                                                                                                                                                                                                                                                                                                                     TOAM:AATOTTAGTATCAATTGGGGAATCATTCGGGAOTTOTGAGAAGTTOCAGAAAATA 2388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTTACAAGTTTCCTAGTTCACCCTTACGGATTCCTGGAGGGAACATCTATATTCACCC
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3349 TTTCTTCATCCAACITATGTTTTAAATGAGGATTATTGATAGT 3392
                                                                                                                        3289 TACTATCATACTGAAACAGATTTCATACCTCAGAATGTAAAAGAACTTACTAATTAT
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                                                                                                                                                                                                                                              3007 AATTACTAATTTTACACATTAGATTTTATTTTACTATIGGAATCTGATATAGTGTTGCT
                                                                                                                                                                                                                                                                                                                                                                      3109 APTCACCAAAATTATCCTGAACTCTTCTGCAAAAATGGATATTATTAGAAATTAGAAAAA 316
                                                                                                                                                                                                                                                                                                                                                                                                              2887 ATGAACACCCTTAGAAAATGTGTCCTATCTALCALCCAAALGCAAITIGATLGACLGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2767 GCCCFAGAGTGGGAGTCCTGATAAGCCAGGCCTGFCGACTACTFFGCCFFCFFFFLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2689 ATGTGACTGTATAACTTTCCCAGGTTCTGTTTATGGCCACALILAALALCITCAGCTCL _=748
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                                                                            TGTTTTATAAAATTTTGCTTTTAATTAAATAAAAGCTGGAAGCAAAGTATAACCATATGA
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Xu,H.:J., Hu,S.-X. and Benedict,W.F.
Broad-spectrum tumor suppressor genes, gene products and methods
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tumor suppressor gene therapy
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                                                                          784 TTTCAGTTAATGCTATGTGTCCTTGACTATTTATTAAAAGTCTCAGCTGGCATGTTGGTG
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                                         AATCITTCTAAACGATACGAAAGAATITAICITAAAAAIAAAGAICIAGAIGCAAGATIA 849
                                                                                                                                                                                                                                                              GTTCTCTGIAAAGAACAFGAATGTAATATAGATGAGGTGAAAAATGTTTATTTCAAAAAAT 1023
                                                                                                                                                                                                                                                                                                                                     GFFCFCTGTAAAGAACATGAAFGTAATAGATGAGGTGAAAAATGTTTATTTCAAAAAT 729
                                                                                                                                                                                                                                                                                                                                                                                                    GGTCAGAACAGAAGAGGGATAGGAAAACAAGTAGAAAATGATACAAGAATTATTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAGAACCATATAAAACAGCIGIIAIIACCCAIIAAATGGTTCACCICGAACACCCAGGCGA 609
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       Antelman,D., Gregory,E.J. and Wills,K.N
Retinoblastoma fusion polypeptides
Patent, US 6074850-A 3 13-JUN-2000;
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Antelman.D., Gregory
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2164 TTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAAUGAGIAIGAACICATG
                                                                                                                                              2104 CGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCTGTGTGAGCAYCCAGAA
                                                                                                                                                                                                                     1810 CGGCTAGCCTATCTCCGGCTAAATACACITIGIGAACGCCTTC1GFCTGAGCACCCAGAA 186
                                                                                                                                                                                                                                                                                        2044 TTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTCACTGTTTTATAAAAAAAGGGTAT 21-4
                                                                                                                                                                                                                                                                                                                                                           1984 AAAGGTTCAACTACGCGTGTAAATTCTACTGCAAATGCAGAGACACACAAGCAACCCCAGCC
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1264 ACCACTOTTATCAACACTATCCAACAATTAATCATCATTTTTAAATTCACCAACTGATGAA 1323
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2224 AGAGAGAGGCATTTIGGAGCAAATTATGATGTGTTTCCATGTATGGCATATIGGAAAGTGAAG
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TATAACTCGGTCTTCATGCAGAGAGTGAAAACAAATATTTTGCAGTATGCTTCCACCAGG 2169
                                                                                                                                                                                                                                                 AATATAGACCTTTAAATTTGAAAATCATTGTAACAQQATGATAQAAGGATGTTTQCTGCTGTTT 2049
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* REFERENCE

AUTHORS TITLE

Deletions of a DNA sequence in retinoblastomas and mesenchymal

VERSION KEYWORDS SOURCE

ORGANISM

HUMARBALKA 4600 bp mRNA linear FP: 12 JHL 1995
Human retinoblastoma associated (RKI) mRNA, complete cds.
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ALIGNMENTS

ACCESSION

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 GTATGATGTATTGGTTTGCACTCTTCAGGAAATTGGAAAGGACATGTGAACTTATATTTT 428
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TANAETQATSAFQTQKPLKSTSLSSLFYKKVYRLAYLRLNTLCERLLSEHPELEHTIWT
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VRLEFEETEEPDFTALCQKIKIPDHVRERAWLTWEKVSSVDGVL/GVIQKKKFIWGIC
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/note="fetimoblastoma=associated protein"
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REFERENCE

AUTHORS

Young, P.E.,

Eukar yota;

Mammalia; Entheria; Primates; Cafarrhin; Hominidae;

Augustus, M., Carter, K.C., Ebner, F., Endress, G.

Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;

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Detection of heterozygous mutations in the RB1 gene in
retinoblastoma patients using single strand conformation
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}" F64 bilateral familia}	exon 402517 /gene-"RB1" /note-300-118-734" /number-3	exon	Znote-"Timor coeld unilateral mutation causing wrong splice; G00:118-734" /citation-[5] /replace-"t"	Variation 179 // Observable Transfer of Table 179 Variation 179 // Observable Table 179 // Observable 17	TANAETQATSAFÇTQKPLKSTSLSLFYKKYYRLAYLRI.NTI.CERI.LSEHPELEHITWT LFQHTLQNEYELMRDRHLDQIMMCSMYGTCKVKNIDLKEKI.IVTAYKDLPHAVQETFK EVI.TREEEYDS.TTVFYNSVFM.JELRTNII.QYASTPEPTLSETEHITEPS.PYKSPSSELS. IPGGNIIYISPSKEYKI.SEGLEPTEIKMERSEKI.LVS.GES.GUTSKKEVK.NQMYCKSJ	SDQPSBNLISYENNOTVNPRESILKRVKDIGY IFKEKFAKAVGQGCVEIGSQPXKLGV RLYYRWESMI.KSEHERI, SLONFSKILLINDI.FHMSILIACALEVVMATYSRSTSONIJDS GTDI.SFPWILLINIKAFDPYKVIESFIKARGNI.FREMI.KHLEKCEHRI IMESI.AMI.SD GTDI.SFPWILLINIKAFDPYKVIESFIKARGNITKEMI.KHLEKCEHRI IMESI.AMI.SD	ASALTIMMTÖÖLI INMALHALIHALIMASAYINTESKELÄÖLELÄSELELTÄHTÄÄN TORMANTATÖHTÄN TARATATATATATATATATATATATATATATATATA AVOTIONA TÖVE KANSANGERAALIMASINATATATATATATATATATATATATATATATATATATAT	/WILAKET WID INO ITE JAPANAAAAAAAAAAPPAAPPPAPPPEEDPEQDSGPEDLPL /LEAGUSTALLOON_WEPKIPERKTAATAAAAAAAPPAAPPPPPPEEDPEQDSGPEDLPL VRLEFEETEEDDETALCOKLKIPDHVPERAWLIWEKVSSVDGVLGGYIQKKKELWIIC IFTAAVDIJDEMSFIFTEIJÖKNIFTSVHKFFNLIKELDIS KKUNAMSKLIKKKYIVILFA	/producting in a MAB59465.]" /producting in AAB59465.]" /producting in AB59465.]" /db_xref="G1:793995" /db_xref="G1:79394"	/qene_skir /rodon_skirt=1 /mrodinct=1rotinoblastoma_suspectibility_n	CDS 138. 2924		/qene-"RB]" exon 1274	/map="13q14.2" qene 1.,4839		E-mail: brendashailz.eric.on.ca. Location/Qualifiers 1 A830	ratidua Ph; 415 813-5868 FAX: 416 813-4989	Toronto ONT W5G 1X8	Muta	JURRAL Oncovene 9 (5), 1321-1326 (1994) MEDLINE 94203660 PHIMEED 8157792	Partial inactivation of the RB product in penetrance of familial retinoblastoma and	AUTHORS Kratyko, R.A., Otterson, C.A., Hogg, A., Coxon, A.B., Cowoll K and Kayo F (with bilatoral and unilatoral retingblastoms with boliatoral and unilatoral retingblastoms proc Natl Acad. Sci. H.S.A. 90 (15), 7351	TITLE Molocular mochanisms of consequents but there is turned
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/game was /noise=Tamor 608559 mutation causing premature stop.: 000-118-734" /citation=[5]	/note="600-118-734" /note=100-118-734" /number=12 /none-1281"	/citation-[5] /replace="t" /replace="t" 1265. 1352 /geno-"kH1"	/number-ii 1299 /gene-"RHI" /note "Tumor GOS159 unilateral mutation causing a premature stop; GOO-118 734"	/genemkHl_" /genemkHl_" /notemg00-118-734"	/note-"Timor GOS563 unilateral mutation causing premating stop; GOO-118-734" /citation-[5] /replace-"t"	/citation=[5] /replace="t" 1 04	1095 /gene="RB1" /noine="Tumor GoS550 mulation causing premargre stop.; GOO-118-734"	10771185 /qene-"RBI" /note-"G00-118-734" /number-10	1 G Z	/number-8 999. 1076	/gene="RB1" /note="G00-118-734"		0 - " B		0///44 /gene-"RBH" /note-"G00-118-734"	/note-="G00-118-734" /note-=5	/replace="c" 638. 676 /geno="RH3"	premature stop.; G00-118-734" /citation-[5]	/deno="RB1" /note-"Tumor GOS537 bilateral trameshift modulion satisfied	/citation=[5] /replace "ta"	June 77 June 1985 Unitateral transshift mutation Sasing premature stop"	537. 542 (700. 840)	/qene-"RB1" /note"G00-118-734"	Preplace scop (teplace="ca" 518637	

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Query Match
Best Local Similarity
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                                                                                                                 TGAAGTTCTCTGTGTAAAGAACATGAATGTAATATAGATGAGGTGAAAAAATGTTTATTTCAA 1018
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3009 - ОТВАТААЛОСАЛДОСТВТОТВАЛТАЛ ЕТТВДОСТВОТ ЕТТДВАДОСТВИТАЛОСТВА ГОТФТО
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3369 - ААСАЛАТТІ САТАССІСАСААТСТААААĞAAÇITTAÇITGA TTATTTTCITIÇATÇÇAQÇTTA - 3428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3402 CITITAANTIAAATAAAAGCIGGAAGCAAAGTATAACCALAIGAIACTACTACTACIGGA 3461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3222 ATGIGICCIAICIACTACCIICCAMMICCANTITOATIONCIGOCCATION/CANAATTAICC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fukaryota; Mctazoa; Chordata; Craniata, Vertebrata, Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

| (bases 24) to 4740)
| Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y. Human relinoblastoma susceptibility gene. Clouing, identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl Acad S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular mechanism of retinoblastoma gene inactivation in
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Homo sapiens (clone: PR-[1,5]) foetus retina opna to mPNA
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             /gene-"RB1"
                                            /dev_stage="foetus"
1. .4740
                                                                                                            /tissue_type="retina"
                                                                                                                                    /clone="RB-[1,5]"
                                                                                                                                                                         /map-"
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/db_xrei-"taxon:9606"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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719 CITOCATCACATTILIAFIASCIAAASSSSAASIAIIACAAAISSAASAGAIGAASA
                                                                                                                                                                                                 488 CTTGGATGACATTTGTATTAGCTAAAAGGGGAAGTATTACAAALGGAAGATGALCLGGLGA 547
                                                                                                                                                                                                                                                                 659 TGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAAGTLL 71×
                                                                                                                                                                                                                                                                                                                           428 TGACACAACCCAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGGTGGTAAAAATTT 48
                                                                                                                                                                                                                                                                                                                                                                                               599 AGTATGATGTATTGTTTGCACTCTTCAGCAAAITGGAAAGGACATGTGAACTIAIATAT: 652
                                                                                                                                                                                                                                                                                                                                                                                                                             368 ACTATICATETATECHTECACTOTTCAGCAAATTUJAAAGGACATGTGAACTTATATATAT 42°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 TACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTJAAGA Syr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 GTTTCAC-TTTACTCACGACAGAAAAACATACGAAATCAGTGTCCATAAATTCTTTAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 TACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGA (4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 GITCACTTTTACTGAGCTACAGAAAAGATA GAAATCAGTGTCCATAAATTTTTTAACT ↔
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TTGGTIAACFIGGGAGAAAGIFFCATCTGTGGATGGAGIAFTGGGAGGTTATAIICAAAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 TTSOTTAACTTSSSAGAAAGTTTCATCTSCATGGAAGTATTGGGAAGGTATATTCAAAA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 GAAAAAGGAAGTGTGGGAATGTGTATGTTATTGGAGGAGITGAGGTAGATGAGATGAGATGTC 24×
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TANAETQATSAFQTQKPLKSTSLSCH YKKYYKLAYLKUNTLCHKUT SEHPFILHETW!
LEQHTIQNEYFIMREHHTDQTMMQSMYSTQKYKYTETKPYTTYLAYLCHKXXCHXKXXGSTIKVNS
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RVLIKEEEYDSIIVEYNSVEMQELKINILQYASTREPTILSEIFFFERSEYKEFSSELF
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VRLEPEETEEPDETALCQKIKIPHWYEEPAWLTWEKVSSVDSVLSVYIGKKKELW31/
TELAPVCLEMSFILLSYPKIYEISVWEEPAWLTWEKVSIVSVANASELLKKYIVLTH
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/db_x+-t="G1-190959"
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139. .2925
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99.7%;
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1687 1918	5 – 5	ОУ 1628 Db 1859	
1627 1858	ATTA	- -	
1567 1798	010 - 10 - 10 - 10 - 10 - 10 - 10 - 10 -		
1507 1738		υγ 1448 Db 1679	
7 4	3=3		
1387 1618	GCANAVITYTGANATGACANYATTTTTCATATGTCTTTATTGGCGTGCGCTCTTGAGGTTG		
1327 1558	=======================================		
1267 1498	TGGGAV'AGAST IGTGTCGAAATTGGATCAC'AGCGATAC'AAACTTGGAGTTCGCTTGTATT 		
\	GTATACTGAAAAGAGTGAAAGAGATATAGGATACATCTTTAAAGAAATTTGCTAAAGCTG 		
	ATCAACCT ICAGAAAATCTGA FI ECCTALFI LAACAACTGCACAGTGAATCCAAAAGAAA 	1 1	
1087 1318	3=3	1. 1.	
1027 1258	CACTC		
967 1198	CAFTATITITIGA FOATGATAAAACTO FOAGACTGATTOTATAGACACTTTTGAAACAC - - - -	1	
907 1138	TTGAAAAT TEECTAAACGATACGAAGAAATTTATCTTAAAAATAAAGATCTAGATGCAA 	<u> </u>	
847 1078		= .,	
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667 898	"AAAGAACCATATAAAACAGCIGTTATACCCATTAATGGTTCACCTCGAACACCCA	J	

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H.sapiens DNA for 4.6 kb retinoblastema gene probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             retinoblastoma gene probe
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                                   292 CATAAATTCTTTAACTTAAAAGAAATTGATACCASTACCASTACCASTSCATAATGCTATG 351
                                                                                                                   232 GACCTAGATGAGATGTGGTTCACTTTTACTGAGCTACAGAAAAGATAGAAATCACTGTC 291
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Matches 3223; Conservative
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787 ATTCCTCCACACACICEAGTTAGGACTGLIALGAACACIALCCAACAALIAALGALGALGAIT 846
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                                       l (bases 1 to 4242)
Xu.H. J., Bu.S. X. and Benedict,W.F.
Broad spectrum tumor suppressor genes, gene products and methods
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    Mismatches

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2032 HARGCANATGCAAAGTTGAAGAA: ATAGACC FTAAATTCAAAATCATTTTAACAGCATAC 2091 HILLIH	1627 CIGITTATANANANGTGTATCGGCTATATCTCCGGCTANATANANANANACCCC 1686 1912 CITICIGGCTAGACACCAGAATTAGAACATATCATCTGGAACCCTLLLCCAGCACACCCC 1971	1732 CUTGTANGATCTGGAAGAAAAAAGGTTGAACTACGGGGTGAAATTCTAGTGGAATGGA 1791 11507 CUTGTAGAAGAAGAAAAAGTTCTAGAACAAATTCTAGTGGAAATGGA 1556 1792 GAGAGACAAGGCAAGGTCAGACCTTCCAGACCAAGAAGCAATTGAAATCGAACTCTATCATAAAAAAAA	1612 ITATITGATCITAATAAAAATAAGAACGAGAAGAAGGACCAACTGATCACCTTGAATCT 1671	492 TACAAACTGATCGATACTTTTTTTTTTCAAAGCAAACCTTGCATGACAAGAAAATGATTAATAAAA 1 111111111111111111	1087 ICCATTCAAAATTTAACAAACTTCTGAATGACAACTTCTCAGAATCTCAGAATCTTCAGAATCTTGAGCG 1146 1372 TECGCTCTTGAGCTCTTGAACCACACATATACCAGAAGTACATCTCAGAATCTTGATTCT 1431 1147 ICCCCTCTTGAGGTTCTGAATGACCACATATACCAGAAGTACATCTCAGAATCTTGATTCT 1206 1147 ICCCCTCTTGAGGTTCTGAATGACCACATATACCAGAAGTACATCTCAGAATCTTGATTTT 1491 1432 GGAACACATTTTTTCTCCCATGAATTCTGAATGTGATTAAAAACCCTTTGATTTT 1491 141111111111111111111111111111111	HHILLIHIHHHILLIHHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHHILLIHHILIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIHHILLIH
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HILLIH HI	2707 TGTAGCAGATTGTTTGCTCTTGCAAAGTAAAATTGCTGTGGGATTTAATTAA	2812 TTTGTGGATNIAAANTGTGGAGATGCAATTGTTTGGGTGATTCCTAAGCCACTTGAAATG 2821 1111111111111111111111111111111111	TGAGGA	1572 AAACATCTCCCAGCAZACTCCAAATTTCACCAGAAACTGGATAGAAATGACTATA ACTAGA HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	2452 AATTAANISETATETAACASESTATESTICAAAAASIASIAAASIAAASIAAA OO 2511 11111111111111111111111111111111	1927 TATGATTCTATTATAGTATTCTATAACTCGGTCTTCATGCAGAGACTGAAAAAAAA

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                                                                                                                                            2810 FCACCICCAACACCCAGGCGAGGICAGAACAGGAGTGCACGGAIAGGAAAACAACTAGAA 2751
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                                                     712 AATGATACAAGAATTAITGAAGTTCTCTGTAAAGAACATGAATGTAATATAGATGAGGTG 771
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                                                                                                                                                                                                                                             TOACCTEGAACACCCAGGCGAGGTCAGAACAGGAGTGCACGGATAGCAAAAACAACTAGAA 711
                                                                                                                                                                                                                                                                                                                                    CTCTCACCICCCATGTIGCTCAAAGAACCAIATAAAACAGCIGTTATACCCATTAAIGGT 281
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Patent: US 5496731 A 2 05-MAK 1996;
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Xu.H. J., Hu.S.-X. and Benedict, W.F.
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Let, M.-H. and Lee, E.Y.-H.P.
Reilnoblastoma gene cancer suppressor and regulator
Patent: US 5998134-A 4 07-DEC 1999;
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Antelman, D., Gregorty, P. i. and wills, K.
Retinoblastoma fusion polypeptides
Patent: US 6074850-A 3 13-JUN 2000;
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                                                                                                                          2469 CAGCGACCG IGTGC ICAAAAGAAGIGC IGAAGGAAGCAACCC ICCTAAACCACIGAAAAA 2528
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660 GACACAGONAGAGI TGATA ETIAGI GAAATAAAT ETIG AT EGGI GOTAAAACTTI C
                                429 GACACAACCCAGCAGCTCGATATCTACTGAAATAAATTCTGCATTCGCATTCGCTAAAACTTTC 488
                                                                  540 ACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATGTAAGACTGTTGAAAAA
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                                                                                                                                                                            309 ACTAAAACKAATIGATACCAGTACCAAASITGATAATGCTATGTCAAGACTSTIGAAGAA
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AR207831
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Patent: MS 6379927-A < 30 APR-2002;
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Antelman,D., Gregory,R.J. and Wills,K.N
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PE 15 NOV-1996 US OBJECTO A FRECTOR SE SPROTONE DE DOUGLAS ANTEMAN, RICHARD J CHESTOR KENNETH N WILLS DE COTHEN OFFICE ACLE BEST ANTE STORE DE STEADNERSES SINGLES

CC TOPOLOGY: Linear:
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Tissue specific expression of refinoblastoma protein
Fatent: JF 20015036-88 A 2-21 MAR 2001;
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2648	2589 ST CAAATTCAGCAGAAACTGGCAGAAATGACTCTACTCGAACACGAATGCAAAAGCA	ĸ
	N 2529 MCTACGCTTTGATATTGANGATONGATGANGCAGATGGAAGTAAACATCTCCCAGGAGA :	2 c
	24.69 PARCHAPPER DIRECTICANAMAGARE FOCTSANCEAGCGAGCGUCCTANACCACTGAAAAA THE FILL FILL FILL FILL FILL FILL FILL FIL	F 3
	y 2409 aattgetgaatcattcgggacttetgagacettccagaaaataaatacacaceggatgtaa : 	P 9
2408 2639); 2349 AATTICAGAAGGTCTGGCAACAACAAAAATGACTGCAAGATCAAGAACTTAGTATC: 	g e
2348 2579	y 2289 FTCACCCTTACGGAFTCCTGGAGGGAACAFCFATATTTCACCCCTGAAGAGTCCATATAA : 	2 9
	Py 2229 CAGGCCCCTACCTTGTCACCAATACCTCACATTCCTCGAAGCCCTACAAGTTTCCTAG {	B &
2228 2459	NY 2169 ATTOTATAN'ITCAGTOTTCATGONGNOTAGANANCANATATTTTCONGTATGGETTCONC 	E 49
	NY 2109 PETERARRAKANANANTINAAARONGI PETERAPCAAAGAAGAAGAAGAAGAATAIGATICITATIKATAGI 	da An
	BY 2049 GANGANTATAGACCTTAAATTCANAATGATTGTAACAGGATACAAGGATCTTGCTCATGC	<u> </u>
2048 2279	N 1989 CATSAGAGACAGGCATTTGGACCAAATTATGGATGTGTTCCATSTATGGCATATGCAAAGT 	9G 49
1988 2219	NY 1929 AGAATTAGAACATATCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATGAACT 	<u>g</u> c
1928 2159`	DY 1869 STATCGGCTAGCCTATCTCCGGCTAAATACACITIGTGAACGCCTTCTGTCIGAGCACCC	qa An
യ് ത്	29 1809 AGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAGT	ž Š
ŭ 6	UY 1749 GAAAAAAGGIICAACIACGCGIGIAAATICIACIGCAAAIGCAGAGACACAAGCAAGCACCIC - - - - - - - - - - - - - - - - - - -	# S
	QY 1689 TCCTCTCCASAATAATCACACTSCASCASTATATSTATTCTCCTCTATAASATCTCCAAA 	F 5
1688 1919	Qy 1628 AGANTGAAAGGACCGAGAAGGACCAACTGATCACCTGGATCTGCTTGTCCTCLLTAALCI 	F 5
	UY 1569 ACAICCAAICAFGGAATCCCTTGCAIGGCICTCAGATTCACCTTTAITTGAICTTATTAA 	₽ C
1799	Db 1740 TITTATCAAASCAGAASGCAACTTGACAASAGAAATGATAAAAACATTTAGAACGATGTGA	豆

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Scoring table:
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Pred. No. is the number of results predicted by clause to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		утегу Оцегу				
- 23	Score	Match	Length	123	110	Lorser Liptical
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κ.	4797	100.0	2994	J .	AR098189	ARCON CAS SALES
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Abtelman, D., Greecry, R.J. and Wills, K.N.
Tissue specific expression of retinoblastoma protein
Patent, JP 2091503638 A 2 21-MAR-2001;
CANJI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa:
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TANAETQATSAEQTGKPLKSTSLSLFVKKVYRLAYLFLNIL/EF/LLSEHFELEHTWI
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NET LATENATA VEGENORIA DE ASLATEN ASTATORIA DE SESSA TEMBAST STATESTE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE SESSA TERMA DE 
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VKLIEFETEEPPTALOQKLKIPDHVREFAWLIWEKVSSVIFYOTTOKKKEIWITT
IFTAAVDIJJEMSFTFTELQKNIPTSVHFFFNLEKE OTSTEVONAMSKLIKKYDVLEA
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/db_xrei="dI:190963"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TECHT FÖNERETIMEDER HAD TIMESMEGT CKAR UTT FER FLANKTERBANDETER
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae; Homo.
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                                    /cell_type="retinoblast"
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                                                                                                                   161 LouPheSerLysLouGluArqThrCysGluLouTLeTyrLouThrGinFroSerSerEar 180
                                                                                                                                                                                                           424 AGIAGCAMAGITGATAMTGCTATGTCAMGACTGTTGAMGAMGAMGATGTTGTATGTTTGCA
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                                                                                                                                                                                                                                                                                     141 SerThrLysValAspAsuAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 160
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Draft entry and computer-readable copy of sequence in [1] kindly provided by R.Bookstein, 27-APR-1987.
                                                                                                       Molecular mechanism of retinoblastoma gene inactivation retinoblastoma cell line \mathbf{Y79}
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106 AlaAlaValAspLeuAspGluMetSerPheThrFheThrGluLeuGluLysAsulleGlu
                                         182 ATACCAGATCATGTCAGAGAGAGAGCITGGTTAACITGGGAGAAAGTTTCATCTGGAT 241
                                                                                                                                                                                                         122 A3631 GAGTITGAGAGAAGAGAGAAGAGGTGAITITAGTGCAITAGTGCAGAGT AGAAATTAAAG TB
                                                            86 GlyVall.co51y51y19y11e61o1y31y31y351o1.co11p61y11e6ys11e4he11e-10f
                                                                                                                                                             66 HeProAspHisValArgOluArgAlaTrpLouThrTrpOluLysValSetSetValAsp
                                                                                                                                                                                                                          46 ArqLeuGluPheGluCluThrGluGluFroAspPhoThrAlaLouCysGlnLysLouLys 65
                                                                                                                                                                                                                                                                                       62 CCGCCCCCTCTTGAGGAGAACCCAGAGAGAGAGAGAGCGGCCGGAAAACCTTACCCTTCTCTTCTTCTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    retinoblastoma gene probe
Patent: EP 0293266 A 1 30 NOV-1988;
RESEARCH DEVELOPMENT FESHIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \Lambda method for detecting the predisposition to retinoblastoma and a method for detecting a retinoblastoma gene in tumors using a
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325 961	ValThr GTAACA	10b 9
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265 781	11eA5n0 111111 A11AA10	
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12 E -	706 CysSerMetTyrGlyileCysLysValLysAssiloAspLenLysPheLysIlcileVal 	рь
	686 HisThriquGlnAsnGluTyrGluLouMetArgAspArqHistouAspGlnLloMetMet HIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	Qy Db
685	666 CysGluArqLeuLeuSerGluHisProGluLeuGluHislle1leTrpThrLeuPheGln 	Qy Db
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64°. 1920	626 AlaAsnAlaGluPhrGinAlaThrSerAlaPheGinThrGinLysProLouLysSorThr 	Qy Db
186.	606 TyrLeuSerProValArqSerProLysLysLysGlySerThrThrArqValAcaSerThr 	Qy Db
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CHIKYU KANKYO SANGYO GLUUTSU KENKYU KIKO
OS Mus uniscultis (moise)
PN JP 1997023884 A/1
PD 28 JAN 1997
PF 14 JUL-1995 JP 1995177741
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             921 AspThrSerAsnLysGluGluLys 928
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Search completed: January 18, 2003, 22:12:26 Job Lime : 4176.34 secs

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ONITS-bits STAPF:1 -PND=1 -MATFIX=130 -MINMATCH=0.1 -0.00PCI=0 -0.00PEXIT-0

ONITS-bits STAPF:1 -PND=1 -MATFIX=100 -THK_MIN-0 -ALIGN=15 -MODE-LOCAL

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em_htgo_other:*	41:	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	81	10	Description
	.7	94.9	2994	ē	AK091965	Akus) 965 Sequence
t.)	4273	99.9	2994	ç	AK098189	
نب		99.9	2994	্ৰ	AR207831	
4	4273	99.9	2994	3	BD009728	
UT.	27	99.9	2994	÷	181465	181465 Sequence
5	27	99.9	2994	ۍ	HUMRBSA	M28419 Buman retin
7	27		4547	œ.	105311	Something [[Ego]
œ	4273	99.9	4600	÷	HUMRBA I KA	
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10	4273	99.9	4839	Ş	HUMRBIMENA	1.41870 Homo Sapien
11	4266	99.7	4597	œ	109369	IO9369 Sequence
13	4263	99.6	2995	'n	AR144797	AP144797 Sequence
بد ۔	4225	98.8	4740	ç	HUMRHS	MIS400 Human retin
1.1	4213		3232	Ģ	AR072011	AK072041 Sequence
e 15			3232	ç	AR972032	AR0720 (2) Sequence
	4213		3232	5	118496	I18496 Sequence
c 17	4213	98.5	3232	6	118497	118497 Sequence
18	4152		4580	6	A01444	Abl444 II Saptens b
19	3964.5	92.7	4591	6	E12560	
<u>د</u>	3956.5		4591	-	MUSETPLOSKH	M26391 Monse retin
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31	790	18.5	3960	ĵ.	HUMP167B	L14812 Human retin
32	789	18.4	4130	ۍ	AX281827	AX281827 Sequence
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ا ان د	1 ~		8083		AR978225	AROZBILI Sequence
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RESULT 1

ALIGNMENTS

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582 HisilelleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMe: ArqAs;	562 AlaTyrLeuAsnThrLeuCysGluArgLeuSerGluHisProGluLeuGlu Sri 	542 Thr Cludys Prolectlys Set The Set Lea Set Lea Picty Flysbys Vallyr Argical 54 in the Hill Hill Hill Hill Hill Hill Hill Hil	SerIngineArgyalAsnSerIngAlaAsnAlaGiuThrGinAlaThrSerAlaPheGlib 54	ASTASTHISTITTA (AN AASPMECLYTLESSETTFOVALARISETTFOLYSLYSLYSLYSLYS) HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	AspargCluClyProffbraspHisLouGluSerAlaCysProLenAstiLeuProLeuCli-5 AlphargCluClyProffbraspHisLouGluSerAlaCysProLenAstiLeuProLeuCli-5 LITHTHITHTHITHTHITHTHITHTHITHTHITHTHITH	MetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGluSerLys 	442 AlaGluGiyAsnicuThrArgGiuMetileiysHisLeuGiuArgGysGiuHisArgIle 46) 	LewasnVallewasnLeuLysalaPheaspPheTyrtysVallleGiwSerPheTetys 44	2 TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerFheProTrplle 4	382 ASNASPASDILEPHOHISMCTSETLEULEUALUCYSALULEUGIUVULVALVALMETALULET 401 [HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	462 GluScrMetLeuLysSerGluGluGluArgleuSerHeGlnAseBbeSerlysFeuLeu (9) 	-i - i	R22 ArgVallySASpileGlyTyriLicPhetySClugsPheAlitySAlidVal31yGiboly 44) 	392 GluashicuileScrtyrPhcAsnAshCysThrValAshIreLysGluScrtleLeulys 323 	282 ValMetAsnThrileGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnFroSer 301 	262 ArglysSerAssileuAspGluGluValAssiVallieProProHisThrProVaiArglhr 281 	242 ASPHISASPLESTATIONG INTERASPSORT LEASPSORT PROCESSES IN GRANDAR PROCESS INTERACTION OF THE PROCESS IN THE P	222 SertysArgTyrGluGluIleTyrLeuLysAsnLysAspLeuAspAlaArdLeuFheLeu 241

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KEYWORDS
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Antelman, D., Gregory, R.J. and Wills, K.N.
Retinoblastoma fusion polypeptides
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62 LeuPheAlaLeuPheSerlysLeuGluArgThrCysGluLeulleTyrLeuThrdInPro
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                                                                                                           LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnPro 81
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   Homo sapiens
                                                                                                               M28419.1 GI.190962
                                      Homo sapiens retinoblastoma cDNA to mENA
                                                                            retinoblastoma protein; retinoblastoma susceptibility prot\epsilon
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REFERENCE JOURNAL MEDLINE PUBMED

The retimoblastoma susceptibility gene encodes a nuclear phosphoprotein ussociated with DMA binding activity Nature 329 (6140), 642-645 (1987) Kukaryota, Metazoa; Chordata, Craniata, Vertebrata: Enteleostemi
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2994)
1.69.W.H., Shew, T.Y., Hong, E.D., Sery, T.W., Donoso, L.A., Young, L.D. 88014238 Bookstein, R. and Lee, E.Y

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                                                                                                                                                                                                     82 SerSerSerTleSerThrSluffeAsnSerAlaLeuValLeuLysValSerTrpIleThr 101
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                                                                           TTTTATIAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG
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                                                                                                                          PhoLouLouAlaLysGlyGluValLouGluMetGluAspAspLeuVallleSerPheGln
                                                                                                                                                                                                                                                                         FTGTFTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAAACCC 669
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RVL I KEEEYDS I IVFYNSVFMQRLK IN I LQYASTRPPTI SPI PHI PRSPYKFPSSPLR
I PÜÖN I YI SPLKSTYKI SEĞLTI IV I KMI PRSKI LVSI GERSEĞTSEKFQK I NQMVCNSD
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GTDLSSPWILKVLNLKARDEYKYIESFIKAGENITAREMIKHLEBYEHRIKESLAWISD
SPLEDLIKOSKORGEPTIHLESACPLMILPLOMINITAADMYLSBYRSPKKMGSSTPRVS
TANAETQATSAFQIQKPLKSTSLSLFYKKYYRLAYLRLNTLCERLLSEHPELEHIIWT
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/db.xret="d1:190963"
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TCTAAACGATACGAAGAATTTATCTTAAAAAATAAAGATCTAGATGCAAGATTATTTTG
                                                                                                                                                       COLFTEATGAATTOTOTTGGAACTTGTAACATCTAATGGACTTCCAGAGGTTGAAAATCTT
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Dryja,T.P. and Friend,S.
Human DNA in the diagnosis of retinoblastoma
Fitent, EF 6259031-AC 1 09 MAE 1988;
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2091 2091	His flelleTrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 	£ 8
581 2031	AlaTyrtzvuArgizvuAsniThrt.euc'yscTuArgizvutcuSerGTuHtsProGTuLcuuGTu 	£ 6
561 1971	ThroLinLysProLouLysSorThrSorLouSorLouPhoFyrLysLysValTyrArgLou 	441
4 1	SerThrThrArqVallAsnSorThrA aAsnA aG cThrG nA aThrSorA aPhoG n 	£
521 1851	ASHASHHISTITATAATAASPMETTYTLEUSETPTOVATAYGSETPTOLYSLYSLYSLYSLY 	90
501 1791	ASPATGG LUG1yProThrAspHistenG LuSetAlaCysProLeuAsnLeuProLeuGIn 	44
481 1731	MetGlusertenAlaTrpLeuserAspserFroLeu£heAspLeuIleLysGluserLys 	£ &
461 . 1671	AlachuchyAsubeuthraryGluMetiletysHisbeudluArgCysGluHisArgile 	₽ 4 5
441 1611	LouAshVallouAshLouLysAlaPhoAspPhoFyrtysVallleofluSorPhoFletys 	941 An
421 1551	TyrSerArqSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTrpIle 	₽ Ş
401 1491	ASBASPASBILOPBOHISMOTSOTLOULOUALGOYSAFALOUGHUVAIVAIMOTATATBY HILLIHILIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	95 55
381 1431	luSerMetleulysSerGluGluGluArgleuSerlleGlnAsnPheSerlysLeuleu HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	상
361 1371	GysValGluILeGlySerGlnArgTyfLysLegGlyValArgLegTyfTyfArgValMet 	95 A
341	AFTYVALLYSASPILLEGTYTYT LLEPHELYSCIBLYSPBEALALYSALAVALGTYGLEGTY 	흎 중
321 1251	GluAsnLeuilleSetTytPheAsnAsneysThtValAsnPtoLysGluSetilleLeuilys 	팔
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                                                                                Draft entry and computer-readable copy of sequence for [1] kindly provided by S.H.Friend, 10-FEB 1988.
                                                                                                                                                                     Li,F.P. and Weinberg,R.A.

Deletions of a DNA sequence in retinoblastomus and mesenchymal fumors: organization of the sequence and its encoded protein Proc. Natl. Acad. Sci. U.S.A. 84 (24), 9059-9064 (1987)
                                                                                                                                                                                                                                                                                  Eukaryota; Metagoa; Chordata; Craniata; Vertebrata; Enteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4600)
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Human retinoblastoma associated (RB1) mRNA, complete eds
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                           142 Proffyri3/8ThrAlaVallieProlleAsnGlySerProArgThrProArgArgGlyGin 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 CTGTGGGGAATICTGTATICTTTATITGCAGCAGTTTGACCTTAGATGAGATIGTCGTTTCACTTTTT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LewTrp01;11eCys11ePhe11eAlaAlaValAspLewAspGluMetSerFheThrFhe 21
CCATATAAAAACAGCTGTTATATACCCATTAATGGTTCACCTCGAACACCCAGGCCAGGCCAGGTCAG
                                                                                                                 PhoLeuLeuAlaLysGlyGluValLeuGlnMetGluAspAspLeuVallieSerPheGln 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIGHTEGCACHCTTCAGCAAAHTGGAAAGGACATGTGAACTTATATATTTGACACAACCC 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuIleTyrLeuThrGlnPro 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTGAGGTAGAGAAAAAGATAGAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAGAA 414
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                                                                                                                                                                            LeuMetLeuCysValLeuAspTyrPheIleLysLeuSerFroProMetLeuLeuLysGlu 141
                                                                                                                                                                                                                                      THE ATTACT AGCTAAAGGGGAACTA TTACAAATGGAAGA FGATCTGGTGATTTCATTTTCAG
                                                                                                                                                                                                                                                                                                                                                     AGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAGTTTCTTGGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                            SerSerSerHeSerThrGluHeAsnSerAlaLeuValLeuLysValSerTrpileThr 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGATACCAGTACCAAAGTTCATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGTA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspVal 61
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RVLKKSAEGSNEPNPIKNILKEDIEGSDEADGSKHIJEGESKEOOKLAEMTSTRTRMOKO
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TANAETQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHILWT
LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
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MLCVLDYFIKLSPPMLLKEPYKTAVIPINGSPHTPRRGONRSARIAKQLENDTRIIEV
LCKEHECNIDFVKNVYFKNFIPFMNSLGLVTSNGLPEVENLSKPYEEIYLKNKDLDAP
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Horridan,S., Soppet,D.R. and Weaver,Z.
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                                                                                                                                                            Structure and partial genomic sequence of the human retinoblastoma susceptibility gene 80 (1), 119-128 (1989)
Detection of heterozygous mutations in the RE1 gene in retinoblastoma patients using single-strand conformation polymorphism analysis and polymorphism chair reaction sequencing Oncogene 7 (7), 1445-1451 (1992)
                                                               Hogq,A., Onadim,Z., Baird,P.N. and Cowell,J.K.
Detection of heterozygous mutations in the RB1
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142 ProTyrtysThrAlaVallIcProlleAsnGlySerProArgThrProArgArgGlyGln 161
                                                                                                                                                             789 ITAATGCTATGTGTCCTTGACTATTTATTAAACTCTCACCTCCCATGTTGCTCAAAGAA
                                                                                                                                                                                                                                         122 LeuMetLeuCysValLeuAspTyrPheIleLysLeuSerProProMetLeuLeuLysGlu 141
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                                                                                                                                                                                                                                                                                                                                                                    PhelculcuAlaiysGlyGluValleuGlnMetGluAspAspieuVallleSerPheGin 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITTTAT FAGCTAAAGGGGAAGTATTACAAATGGAAGATGATCTGGTGATTTCATTTCAG
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premature stop: GOO-118-734"
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                                             AGGCATTIGGACCAAATTATGATGTGTTCCATGTATGGCATATGCAAAGTGAAGAATATA 2151
                                                                    ArgHisLeuAspGlnTleMe+Me+CysSerMe+TyrGlyIleCysEysValLysAsnIle 621
                                                                                                                                 HisfleTleTrpThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp 601
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                                                                                                                                                                                                                                                                                                          ACCCAGAAGCCATTGAAATCTACCTCTCTCTCTCACTGTTTTATAAAAAAAGTGTATCGGCTA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaGluGlyAsnLeuThrArgGluMetlleLysHisLeuGluArgCysGluHisArglle
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Gregory, R.J., Wills,
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Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Lee,E.Y.
Human retinoblastoma susceptibility gene: cloning, identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular mechanism of retinoblastoma gene inactivation
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Homo sapiens (cione. RB [1,5]) fuctus retina cDNA to mRNA
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Nucl. Acad. Sci. 0 S.A. 85 (16), 601/ 6021
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VBLUEEETHEEPDFTALTQKTKTNOHVRFRAMTWFKVSSV;VIV.003102KKKFTWOTO
                                              /protein_id="AAA69807 1"
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561 2108	541 nThrölnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArqLe 	
5 4 1 20 4 8	ySetThrThrAraValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGl 	
521 1988	nAsnashHisthaldalaAspMottyrLouSorProValarqSorProLysLysLysC - - - - - - - - - - - - - - - - - - -	
501 1928	#ASPAFGFTONLYPEOThrAsplisLenGluSerAladysProLeuAsnLeuProLeuGl 	
481 1868	eMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuTleLysGluSerLy 	
461 1808	SALadludlyAsmLouThrArqdluMetllelysHisLeudluArqdysGluHisArqil -	
441 1748	CLCHASHVAILCHASHCLOULYSALAFHEASPFECTYTLYSVAIILEGIUSETPHEILELY 	
421 1688	rTyrSorArdSorThrSorGlnAsnI euAspSerGlyThrAspLeuSerPheProTrpII - - - - - - - - - - - - - - - - - -	
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361 1508	Y ^C YSVA1SIHI16C1YSerGInAraTyrLySLCSGIYVA1ArqLesTyrTyrArqValMe 	
341 1448	SAL-TVallySASpiledlyfyrilePhelySGlulySPheAlalySAlaValGlyGlnGl 	
321 1388	rGluAsuLeuIleSerTyrPhvAspAsuCypThrValAssProLysGluSerIleLeuLy 	
301 1328	rValMetAsmThrIledIndlut.euMetMetIleLeuAsmSerAlaSerAspGlnProSe RTH DTH	
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LFILDHDKILQTDSIDSEIQRITEKKSNLDEEVNVIPHPTPVRTVMNIT.QQIMMILINSA
SDQPSTMILISVENN'ITVNEKESILKEVKENIYYI.FKEKFAKAVAGAYVELIASQIPYKLAV
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VRLEFEETEFPDFTALCQKLKIPDHVFEFAWLTWEKVSSVDGVLGGYIQKKKELWGIC
IFIAAVDLDFMSFTETFLQKNIEISVHKEFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
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                                              1450 GACCGACAACCAACCGARCTGARCTGCTTGCTCCTCCTCCTAATCTTCCTCTCCAC 15-ex
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FCIFCHACACCTCTGGACTTCACTGACTGACTGTATAACCTTTCCCAGGGTTC 2589
                                                                                                              GATAGCATGGATACCTCAAACAAAGGAAGAAATGAGGATCTCAGGACCTTGGTGGACAC
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Mechanisms of oncogenesis in patients with familial retinoblastoma
Br. J. Cancer 68 (5), 958–964 (1993)
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Detection of heterozygous mutations in the RBI gene in
retinoblastoma patients using single-strand conformation
                                                                                                                                                                                                                                                                                                                     Cowell,J.K. and Kaye,F.J. Partial inactivation of the RB product in a family with incomplete \theta
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                                                                                     FAX: 416 813-4989
                                                                                                                                                  Toronto ONT W5G 1X8
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                                        -mail: brenda™haliz.eric.on.ca.
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LFQHILQNFYFLMFTFHILGIMM:SMYGICKVKNIDLKKYLIVIAYKDLPHAYQETFK
PVLIKEEEYNSIIVFYNSVFMQBLKTNILQXASIRPPTLSPIPHIPRSPYKFPSSPLR
PQGNIYISPILKSPYKISEGLIFFTKMIFKSKILVSIGESKFQKILAEMTSTRTRMQKQ
KVLKKBAAEGSMPPKFILKKLFFFFIRGSDEADJSKHLPGESKFQKILAEMTSTRTRMQKQ
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SPLEDLIKQSKDREGPTDHLESACPI.NI.PI.QNNHTAADMYI.SPVRSPKKKGSTTRVNS
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/citation=[5]
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/citation=[5]
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VRLEFEETEEPDETALCGKLKIPDHVEERAWLTWEKVSSV[WVLGGYIGKKKELWATC
IFLAAVDLDEMSFTFTELGKNIELSVHKEFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
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/product="retinoblastoma suspectibility protein"
/protein_id "AAH59465.1"
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1352. .1375
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Dryja,T.P. and Eriend,S.
Human DNA in the diagnosis of retinoblastoma
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-	1629 1911	DY 1570 TOANCTN'GCGTGTANATTCTN'TGCNANTGCNGAGACACANGCANGCTCAGCGTTGCAG 	<u> </u>
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                                                                                                                                                                                                                                                                                                                                                                                          AATGACAACATTTTTCAFATGTCTTTATTGGCCGTGCGCTCTTGAGGTTGTAA1GGTCACA 14+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2632 CATATHUAAGGATGAAGATGAAGATGAAATTAAAAGATGTCCCAAGGAGAGAGTCCAAATTT 2691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2572 GTGCTCAAAAGAAGTGCTGAAGGAAGCAACCCTCCTAAACCACTGAAAAAACTACGCTTT 2631
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2590 Totttatogocacatttaatatetteagetetttteteegatataaaatgtgeagatgea 2649
                                                                                                                                                                           2530 FORGIACACTOTIGIA FIGA FIGIOTIC FCACAGATGI GACTOTALAACTITICCCAGGITIC 2589
                                                                                                                                                                                                                                                      2752 GATAGCATGGATACCTCAAACAAGAAAAAAAAAATGAAGATCTCAGGACCTTGGTGGACAC 2811
                                                                                                                                                                                                                                                                                                                                         2470 GATAGMATGGATAMMTAAAMAAAGGAAGAMAAATGAGGAMMTAAGGAMMTGGTGGAGAAC 2529
                                                                                                                                                                                                                                                                                                                                                                                                                            2692 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAATGAAATGAAT 2751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2410 CAGCAGAAACTGGCAGAAATGACTTCTACTCGAACACGAATGCAAAAGCAGAAAATGAAT 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2350 GATATTGAAGGATGAAGGAAGGAAGTAAAGTAAAGATGTGCGAGGAGAGTGCAAATTT 2409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2230 TCATTCGGGACTTCTGAGAAGTTCCAGAAAATAAATCAGATGGTATGTAACAGCGACCGT 2289
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Proc. Natl. Acad. Sci. U.S.A. 85 (16), 5017-5021 (1988) 88320373	Molecular mechanism of retinoblastoma gene inactivation in retinoblastoma cell line Y79	, Lim,C.J		87149066	J,	omiq,L.J., Shew,J y genes closing,	Edikaryota; Motazoa; Chordata; Craniata; Vertebrata; Directeostom;; Mammalia; Butheria; Primates; Catarrhich; Homenidae; Home.	tus ret	M15400.1 G1:190958	Y mRNA, complete eds.	THE NAME OF THE PARTY OF THE PA	TGAGGATTATTGATAGT 3548	TGAGGATTATTGATAGT 3266	ATACCTCAGAATGTAAAAGAACTTACTGATTATTICLICA1CCAACTTATGTTTTTAAA (5 d)	ATACCTCAGAATGIAAAAGGAACTTACTGATTATTTTTCTTCATCCAACTTATCTTTAAA 3249	AATAAAAGCTGGAAGCAAAGTATAACCATATGATACTACTGAAACAAATTTC 471	AAAAGCTGGAAGCAAAGTATAACCATATGATACTATCATACTACTACAAACACACATT		TACTATTGGAATCTGATATACTGTGTGTTTTTATAAAATTTTGCTTTTAALTA	TGCAAAAATGGATATTAGAAATTAGAAAATAGTAAATTACTAATTTACACATTAGATTTT * «%]	AAAAATGGATATTATAGAAATTAGAAAAAAATTACTAATTTACACATTATATATT	TOTATOTTOTAAATGAATITAATIGAATIGAAGAATIAAAAATATOTGAAAYTOTTO 4291	ALIAATIIAIA GUALAITIIIIAA IIIAA A GAACA CAACATIA GAAAA GUGTA	TATTAATTIAIATGTATATTTTTTTAATTTAAACAGAACACCCTTAAGAAAATGGGCCTA Z949	AGGCTGTGTGACIACILIGCCLICILIGIAGCAIAIAIAGGIGAIGLIGCTG LIGTTTT (17)	AGGCCTGTCTGACTFTTGCCTTCTTTTGTACATALAGGTCAIGTTGCCTCTGTTTL 28H9	TAMAATTGETGTGETITATGGATAGTAAGAATGBEECLAGAGTGGGAGAECTGATAACCC (1]]	TAAAATTGCTGTGCTTTATGGATAGGAAGAAGAAGGGCCLAGAGGGGAGGCCTGATAAA CCC 2829	AAAATCTTGTGTAAATCCTGCCATTTAAAAAGCTGTAGCAGATTGTTTTTCTATTTCAAAGC-4051	AAAATCTTGTGTAAAATCCTGCCATTTAAAAAGTTGTAGCAGATTGTTTCCTCTTCCCAAAG 2765	ATTGTTTGGGTGATTGCTAAGCCACITGAAATGTTAGF AIIGTTATFIALLITHTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT		HITTATGSCACATITAATAICHUHHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

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                                    369 STIAATGCTATGTGTCCTTGACTATTTTATTAAACTGTGACCTGGCA1G11GGTCAAAAAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 CTGTGGGGAATCTGTATCTTTATTGCAGCAGTTGACCTAGATGAGATGTCGTTCACTTT 69
                                                                                  ATTITITATIVAGCITAAAGGGGGAAGITATIVAGAAATGGAAGATGATIGTGGTGATITITCATITICA 788
                                                                                                                                                                                       CAGCAGTTCGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAAGTTTCTTGGATCAC
                                                                                                                                                                                                            AATTGATACCAGTACCAAAGTTGATAATGCTATGTCAAGACTGTTGAAGAAGTATGATGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGAGCTACAGAAAAAACATACGAAAATCAGTGTCCATAAATTCTTTAACTTACTAAAAAGA
                                                                                                                                 ATTITIATIAGCIAAAGGGGAAGTATTACAAATGGAAGATGATCIGGIGAITICATITCA 368
                                                                                                                                                                                                                                                                                    ATTGTTTGCACTGTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAAGC
                                                                                                                                                                                                                                                                                                                                  ATTGTTTGCACTCTTCAGCAAATTGGAAAGGACATGTGAACTTATATATTTGACACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACIGAGCTACAGAAAAACATA-GAAATCAGIGTCCATAAATTCTTTAACTTACCTAAAAGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGTGGGGAATCTGTATCTTTATTGCACGAGTTGACCTAGATGAGATGTCGTTCAC-TTT 488
            brail entry and computer readable ccp; of sequence in [1] kindly provided by R.Hookstein, 27-APR-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038
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- bp upstream of FooPI site: chromosome 13q14.1-q14.2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPGGNIYISPLKSPYKISEGLPTPTKMTPRSRILVSIGESFGTSEKFQKINQMVCNSD
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CUDI.SFPWII.NVI.NLKAFDFYKVIESFIKAEGNIJTREMIKHJERCEHRIMESI.AWI.SD
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SDQPSENLISTFNNCTVNPKESILKRVKDIGYIFKFKFAKAVGQGCVFIGSQPYKLGV
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VRLEFEETEEPDETALCQKLKIPDHYRERAWLTWEKVSSVL%VLGGYTQKKKELWATC
IFIARVDLDEMSETLLSYRKTYEISVHKFFNLLKEIDTSTKVDNAMSRLLKKYDVLFA
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/db_xref="G1:190959"
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/product="rbs_mRNA"
139, .2925
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Broad-spectrum fumor suppressor genes gene products and methods
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                                                                                                                                                                                                         283 FIGGIGCIAAAAGITICITGGA ICACA FELITA KTAGCTAAAGGGGAAGIA ITACAAATG 342
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  l (bases I to 3232)
Xn.H. J., Hu.S. X. and Benedict,W.E.
Broad-spectrum tumor suppressor genes, gene products and methods
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Xu.H.-J., Hu.S.-X. and Benedict,W.F.
Broad spectrum tumor suppressor genes, gene products and metro-ds
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Patent: EF 0293266-A 1 39-NOV-1988;
RESEARCH DEVELOPMENT FOUNDATION
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Fung,Y.K.T., T'Ang,A., Murphree,L.A. and Benedict,W.F.
A method for detecting the predisposition to retinoblastoma and a
method for detecting a retinoblastoma gene in tumors using a
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Patent: US 6074850 A 3 14 JUN-2009;
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DOUGLAS ANTELMAN, RICHARD I GREGORY, KENNETH N WILLS PC

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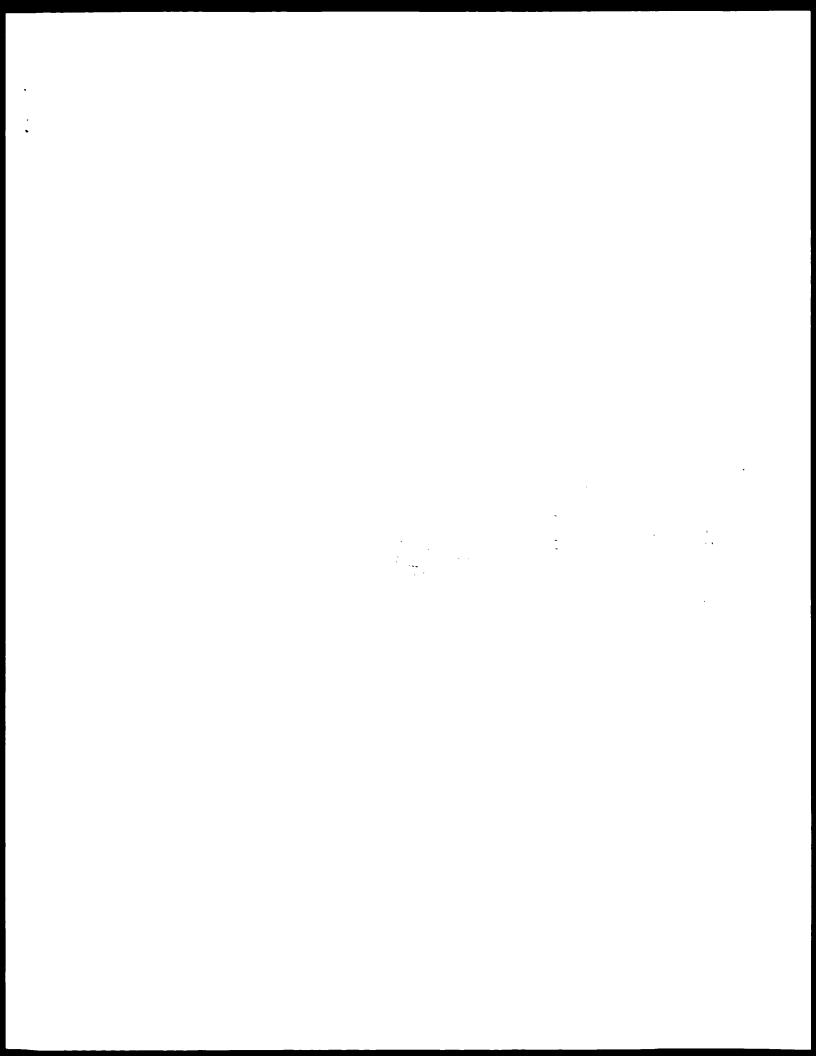
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SUMMARIES

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ALIGNMENTS

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122 LeuLeuAlalysGlyGluValLeuGluMetGluAspAspLeuVallleSerPheGluLeu 141
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                                     673 AGTICGATATCTACTGAAATAAATTCTGCATTGGTGCTAAAAACLLLCLLGGATCACATTI 732
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Characterization of a novel anti-pll0.sup.RR monoclobal antibody
Patent: 98 5710255 A 2 20 JAN 1998;
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                 2 SlutysValSerSerValAspGlyValLeuGlyGlyTyrrleGlntysLysLysGluLeu 21
CAGAAACT FTCATCTGTGGA FGCAG FATTGGGAGG FTATATTGAAAAGAAAAAGGAAGTG
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Harowitz, J.M., Gerber, M.R., Wanq, X.F., Bogenmann, E. Li, E.P. and Weinberg, R.A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Homo sapiens (clone: p4.7R) cDNA to mRNA
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TANABTQATSAFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHPFLEHIIWT
LFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFK
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KMNDSMDTSNKEEK"
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SDQPSENLISYFNNCTVNPKESILKKVNDIGYIFKERFAKAVGGGCVEIGSQRYKLGV
RLYYKYMESMLKSEEERLSIQNFSKILNDNIFHMSILACALEVVMATYSRSTSQNIDS
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LCKEHECNICEVKNYVEKNFIPPMNSLALVTSNALPEVENLSKPYEETYIYNXALDAR
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/translation-"MPPKTPRKTAATAAAAAAEPPAPPPPPPPPPEEDPEQDSGPEDLPL
/translation-"MPPKTPRKTAATAAAAAAEPPAPPPPPPPPEEDPEQDSGPEDLPL
VPLEFEETEHETETTALGGKLKIPGHVVFFAAW.LWEKVSSVINGVLGGYTGKKKLLW7TO
LFTAAVDLDIMKSFTFTELOKNIELSVEKFFNILLKEIDTSTKVUNAMSRILKKYDVLFA
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/db_xref="GI:190946"
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/clone "pd 7F"
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94031584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with bilateral and unilateral retinoblastoma
Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7351-7355 (1993)
94448271
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Gene 80 (1), 119-128 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                    Partial inactivation of the RB product in a family with incomplete penetrance of familial retinoblastoma and benign retinal tumors
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Cowell,J.K. and Kaye,F.J.
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Structure and partial genomic sequence of the human retinoblastoma
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                                                                                                                               Hospital for Sick Children
555 Univ. Ave.
                                                                                                                                                                                                                     Mutation data provided by Dr. B.L.Gallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8346255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular mechanisms of oncogenic mutations in tumors from patients
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wrong splice; G00:118-734"
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Alianment Scores: Pred. No.: Score: Score: Porcent Similarity: Best Local Similarity:		variation	variation	variation	variation exon	variation	exon	exen exon	₹xon
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1392 GIGAAGGAFAFAGGAFACAICHHAAAGAAGAAHFIGGIAAAGCIGFGGGACAGGGFTGT 145
                                                     2412 GTOTTCATGCAGAGACTGAAAACAAATATTTTGCAGTATGCTTCCACCAGGGCCCCCTACC
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                                                                                                                                                     TTCANACGTGT FTTGATCANAGAAGAGGAGTATGATTCTATTATAGTATTCTATAACTCG
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Proc. Matl. Acad. Sci. U.S.A. 85 (16), 6017 6021 (1988) 88320373
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Lee,W.H., Bookstein,R., Hong,F., Young,L.J., Shew,J.Y. and Loc.F.Y
Human retinoblastoma susceptiblity gene. cloning, identification
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provided by P.Bookstein, 27 APE 1987.
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/tissue_type-"retina"
/dcv_stage="foctus"
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/translation="MPPKTPAKTAATAAAAAAEPPAPPPPPPEEDPEGDSGFEDLD
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                                                                                                                                                                   247 TIGGTGCTAAAAGTTTCTIGGA1CACA11111A11AGC1AAAGGGGAAGTATTACAAATG
                                                                                                                                                                                                                                                                                    92 Cys6lsLeg11eTyrLegThr6lsFroSerSerSer11eSerThr6ls11eAssSerAls 111
                                                                                                                                                                                                                                                                                                                                                                                                        72 SerArgLeuLeatystysTyrAspValLeuPbeAlaLeuPheSerLysLeuGluArgThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 CATAAATTCTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAATGCTATG ]26
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1506		144:
5]] 1446	LegPheAspLeptietyseteSertysAspArgetoetysetethraspHisteoglosee 	138
491	HisLeuGluArgCysGluHisArgIleMetGluSerLeuAlaTrpLeuSerAspSerPro	472
1386		1327
471	TyrLysVallleGluSerPhoIleLysAlaGluGlyAsnLeuThrArgGluMet.IleLys	45.
1326	- - - - - - - - - - - - - - - - - - -	126
451	ClyThrAspleuSerPheProTrp://cleuAsnValleuAsnLeuLysAlaPheAspPhe	43.
1266	- - - - - - - - - - - - - - - - - - -	120
431 1206	CysAlaLeuGluValValMetAlaThrTyrSerArqSerThrSerGlnAsnLeuAspSer 	114
411	SerileGlnAsnPheSerLysLeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAla	39
1146		108
391	GiyvalArqLouTyrTyrArqVa:MetGluSerMetLeuLysSerGluGluGluArqLeu	37
1086		102
371	TysPhoAlsEysAlaValGlyGlnGlyCysValGluIleGlySerGlsArqTyrLysLeu	35
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351 966	ValAsnPsoLysGluSerIleLeuLysAsqValLysAspIleGlyTyrIlePheLysGlu 	3 3
331 906	LouAsnSetAlaSetAspClhPtoSetGluAsnLoulloSetTytPhoAsnAsnGysThr 	84 1
311	IleProProHisThrProValArqThrValMetAsnThrIleGlnGlnLeuMetMetIle	29
846		78
291	ASPSerPhe01sThr01nArqThrPr0ArqLysSorAsnLeuAspGluGluValAsnVal	27
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271 726	i-ysaspi.cuAspAldatyleuthel.euAspHisAspLysThileuGliuThiAspScrtle 	66
251	AsselyLeuProGluValGluAssLeuSerLysArgTyrGluGluIleTyrLeuTysAss	23
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231	LyoAssValTysPheLysAssEbelleFigFheMcLAssSeiLeuGlyLeuValThisei	21
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211 5 4 6	ASHASPThrargile:ieGluValleuCysLysGluHisGluCysAshIleAspGluVallHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	19
191 4 หร่	SerProArgThrProArgArgGlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGlu 	17
426	7 CTCTCACCTCCCATGTTGCTCAAAGAACCATATAAAAACAG	36

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